

STIC SEARCH RESULTS

Biotech-Chem Library

Questions about the scope or the results of the search? Contact the searcher or contact:

Mary Hale, Information Branch Supervisor 308-4258, CM1-1E01

Voluntary Results Feedback For	4
> I am an examiner in Workgroup:	Example: 1610
> Relevant prior art found, search results us	sed as follows:
☐ 102 rejection	•
☐ 103 rejection	
Cited as being of interest.	
☐ Helped examiner better unde	rstand the invention.
☐ Helped examiner better unde	rstand the state of the art in their technology.
Types of relevant prior art found:	
☐ Foreign Patent(s)	
Non-Patent Literature (journal articles, conference proc	eedings, new product announcements etc.)
> Relevant prior art not found:	
Results verified the lack of relevant p	rior art (helped determine patentability).
_	g patentability or understanding the invention.
Comments:	

Droploff or send completed forms to STIC/Biotech-Chem Library/GM1/= Girc Desk-





STIC Search Report Biotech-Chem Library

STIC Database Tracking Number: 97246

TO: Nita M Minnifield Location: 1/8a07 & 8e12

Art Unit: 1645

Tuesday, June 24, 2003

Case Serial Number: 002784

From: Edward Hart

Location: Biotech-Chem Library

CM1-6B02

Phone: 305-9203

edward.hart@uspto.gov

Search Notes

Examiner Minnifield,

Here are the results of the search you requested.

Please feel free to contact me if you have any questions.

Edward Hart



STIC-Biotech/ChemLib

From:

Chan, Christina

Sent: To:

Monday, June 23, 2003 1:16 PM Minnifield, Nita; STIC-Biotech/ChemLib

Subject:

RE: rush sequence search

Please rush. Thanks Chris

Chris Chan TC 1600 New Hire Training Coordinator and SPE 1644 308-3973 CM-1, 9B19

> ----Original Message---From: Minnifield, Nita

Sent: Monday, June 23, 2003 12:47 PM Chan, Christina

Subject:

rush sequence search

Christina, please approve, 2 month amdt.

STIC

10/002784

Please do a commercial database search on SEQ ID NO: 16 and 27.

Please a provide paper copy of the results.

Thanks, Nita M. Minnifield Art Unit 1645 Office CM1-8A07 Mailbox CM1-8E12 703-305-3394

Edward Hart Technica, Info. Specialist STIC/Biotech CMI 6B02 Tel: 305-9203

6/03/03 ABSSON 2-AA

WEST Search History

DATE: Tuesday, June 24, 2003

Set Name side by side	Query	Hit Count	Set Name result set
DB = USPT, I	PGPB,JPAB,EPAB,DWPI,TDBD; PLUR=YES; OP=ADJ		
L11	15 and pyrogenic adj5 exotoxin	18	L11
L10	L5 and pyrogenic	18	L10
L9	17 and altered adj10 antigen receptor	4	L9
L8	L7 and altered adj10 class II	4	L8
L7	15 and streptococc\$	77	L7
L6	L5 and streptococc?	13	L6
L5	bacterial adj5 superantigen	197	L5
L4	L3 and superantigen	3	L4
L3	l1 or L2	29	L3
L2	ulrich-robert-g.in.	3	L2
L1	ulrich-robert.in.	26	L1

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END OF SEARCH HISTORY



Search Results - Record(s) 1 through 4 of 4 returned.

1. Document ID: US 20030036644 A1

L8: Entry 1 of 4

File: PGPB

Feb 20, 2003

PGPUB-DOCUMENT-NUMBER: 20030036644

PGPUB-FILING-TYPE: new

DOCUMENT-IDENTIFIER: US 20030036644 A1

TITLE: Bacterial superantigen vaccines

PUBLICATION-DATE: February 20, 2003

INVENTOR-INFORMATION:

NAME

CITY

STATE

COUNTRY RULE-47

115

Ulrich, Robert G.

Frederick

MD

US-CL-CURRENT: 536/23.1; 536/23.7

Full : Title | Culation | Front | Review | Classociation | Date | Retourtive | Sexperiers | Aller Interits | Clause | 1500 | Franc Dase | Israec

☐ 2. Document ID: US 20030009015 A1

L8: Entry 2 of 4

File: PGPB

Jan 9, 2003

PGPUB-DOCUMENT-NUMBER: 20030009015

PGPUB-FILING-TYPE: new

DOCUMENT-IDENTIFIER: US 20030009015 A1

TITLE: BACTERIAL SUPERANTIGEN VACCINES

PUBLICATION-DATE: January 9, 2003

INVENTOR-INFORMATION:

CITY

STATE

COUNTRY RULE-47

ULRICH, ROBERT G.

FREDERICK

MD

US

OLSON, MARK A.

GAITHERSBURG

MD

US

BAVARI, SINA

DILLSBURG

PA

US

US-CL-CURRENT: 536/23.1; 424/184.1, 435/320.1

Fig. | Title | Citation | Front | Severe | Classication | Outo | Religiouse | Sectionses | Attentiones | Fig. | Properties | Properties | Fig. | Properties | Properti

3. Document ID: US 6399332 B1

L8: Entry 3 of 4

File: USPT

Jun 4, 2002

US-PAT-NO: 6399332

DOCUMENT-IDENTIFIER: US 6399332 B1

TITLE: Bacterial superantigen vaccines

DATE-ISSUED: June 4, 2002

INVENTOR-INFORMATION:

NAME CITY STATE ZIP CODE COUNTRY

Ulrich; Robert G. Frederick MD
Olson; Mark A. Gaithersburg MD
Bavari; Sina Dillsburg PA

US-CL-CURRENT: 435/69.3; 435/252.3, 435/252.33, 435/320.1, 435/325, 435/69.1, 435/71.1, 435/71.3, 536/23.1, 536/23.7

Full | Title | Challen | Front | Review | Classification | Data | Reference | Sequences | Attachinents |

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4. Document ID: JP 2002522055 W WO 200009154 A1 AU 9889049 A EP 1105154 A1

L8: Entry 4 of 4

File: DWPI

Jul 23, 2002

DERWENT-ACC-NO: 2000-224177

DERWENT-WEEK: 200263

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TITLE: Nucleic acid encoding superantigen toxin useful as a vaccine and for

diagnosis of superantiqen-associated bacterial infections

INVENTOR: BAVARI, S; OLSON, M A ; ULRICH, R G

PRIORITY-DATA: 1998WO-US16766 (August 13, 1998)

PATENT-FAMILY:

PUB-NO	PUB-DATE	LANGUAGE	PAGES	MAIN-IPC
JP 2002522055 W	July 23, 2002		103	C12N015/09
WO 200009154 A1	February 24, 2000	E	118	A61K039/00
AU 9889049 A	March 6, 2000		000	A61K039/00
EP 1105154 A1	June 13, 2001	E	000	A61K039/00.

INT-CL (IPC): A61 K 39/00; A61 K 39/02; A61 K 39/085; A61 K 39/085; A61 K 39/09; A61 K 39/44; A61 P 31/00; A61 P 35/00; A61 P 37/04; C07 K 14/00; C07 K 14/31; C12 N 1/20; C12 N 1/20; C12 N 1/21; C12 N 15/00; C12 N 15/09; C12 N 15/63; C12 P 21/00; C12 P 21/02; G01 N 33/53; G01 N 33/569

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Search Results - Record(s) 1 through 18 of 18 returned.

1. Document ID: US 20030092894 A1

L11: Entry 1 of 18

File: PGPB

May 15, 2003

RULE-47

PGPUB-DOCUMENT-NUMBER: 20030092894

PGPUB-FILING-TYPE: new

DOCUMENT-IDENTIFIER: US 20030092894 A1

TITLE: Modified chimeric superantigens and their use

PUBLICATION-DATE: May 15, 2003

INVENTOR-INFORMATION:

Abrahmsen, Lars

STATE COUNTRY CITY NAME Antonsson, Per Lund SE Helsingborg Bjork, Per Dohlsten, Mikael Lund Arese Kalland, Terje Lund Hansson, Johan SE Lund Forsberg, Goran

Bromma

US-CL-CURRENT: 530/388.1; 435/7.23, 530/388.8

Full | Title | Citation | Front | Review | Classification | Date | Reterence | Sequences | Atlantineerts |

SE

2. Document ID: US 20030036644 A1

L11: Entry 2 of 18

File: PGPB

Feb 20, 2003

RULE-47

PGPUB-DOCUMENT-NUMBER: 20030036644

PGPUB-FILING-TYPE: new

DOCUMENT-IDENTIFIER: US 20030036644 A1

TITLE: Bacterial superantigen vaccines

PUBLICATION-DATE: February 20, 2003

INVENTOR-INFORMATION:

NAME CITY

STATE COUNTRY

MD US Frederick Ulrich, Robert G.

US-CL-CURRENT: 536/23.1; 536/23.7

Fig. | Title | Chaton | Front | Review | Classification | Date | Reference | Settoerates | Attachments

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3. Document ID: US 20030009015 A1

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L11: Entry 3 of 18

File: PGPB

Jan 9, 2003

PGPUB-DOCUMENT-NUMBER: 20030009015

PGPUB-FILING-TYPE: new

DOCUMENT-IDENTIFIER: US 20030009015 A1

TITLE: BACTERIAL SUPERANTIGEN VACCINES

PUBLICATION-DATE: January 9, 2003

INVENTOR-INFORMATION:

COUNTRY RULE-47 STATE NAME CITY

ULRICH, ROBERT G. FREDERICK MD US US MD OLSON, MARK A. GAITHERSBURG US BAVARI, SINA DILLSBURG PA

US-CL-CURRENT: 536/23.1; 424/184.1, 435/320.1

Full Title Colation Front Sevient Christication Date Reference Seguences Attachments FIRST | Prime Desc | Intoge |

4. Document ID: US 20020197234 A1

Dec 26, 2002 L11: Entry 4 of 18 File: PGPB), 12

PGPUB-DOCUMENT-NUMBER: 20020197234

PGPUB-FILING-TYPE: new

DOCUMENT-IDENTIFIER: US 20020197234 A1

TITLE: Immunologic activities of rhesus cytomegalovirus encoded IL-10 and human

cytomegalovirus encoded IL-10

PUBLICATION-DATE: December 26, 2002

INVENTOR-INFORMATION:

COUNTRY RULE-47 CITY STATE NAME

Schall, Thomas J. Menlo Park CA US US Mountain View ' CA Penfold, Mark Spencer, Juliet Foster City CA US

US-CL-CURRENT: 424/85.2; 424/93.7, 435/372

Full | Filla | Citation | Frant | Sevieus | Classification | Date | Reference | Sequences | Attachments ianac fram Desc Intoge :

5. Document ID: US 6514498 B1

File: USPT Feb 4, 2003 L11: Entry 5 of 18

US-PAT-NO: 6514498

DOCUMENT-IDENTIFIER: US 6514498 B1

TITLE: Modified/chimeric superantigens and their use

DATE-ISSUED: February 4, 2003

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Antonsson; Per	Lund			SE
Bjork; Per	Helsingborg		•	SE
Dohlsten; Mikael	Lund			SE
Hansson; Johan	Lund			SE
Forsberg; Goran	Lund			SE
Abrahmsen; Lars	Bromma			SE
Kalland; Terje	Arese			IT

US-CL-CURRENT: $\underline{424}/\underline{178.1}$; $\underline{424}/\underline{182.1}$, $\underline{424}/\underline{184.1}$, $\underline{424}/\underline{185.1}$, $\underline{424}/\underline{190.1}$, $\underline{424}/\underline{192.1}$, $\underline{424}/\underline{194.1}$

Full | Tiller | Cdation | Finot | Sevieur | Classicopton | Date | Reference | Sectionices | Affectingents |

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6. Document ID: US 6447777 B1

L11: Entry 6 of 18

File: USPT

Sep 10, 2002

US-PAT-NO: 6447777

DOCUMENT-IDENTIFIER: US 6447777 B1

TITLE: Polymerized staphylococcal protein a for treatment of diseases

DATE-ISSUED: September 10, 2002

INVENTOR-INFORMATION:

NAME

CITY

STATE # ZIP CODE

COUNTRY

Terman; David Stephen

Pebble Beach

. Δ COUNTRI

Reiser; Raoul F.

Sarasota

FL

US-CL-CURRENT: 424/184.1; 424/236.1, 424/237.1, 424/243.1, 424/280.1, 514/12, 514/18, 530/350, 530/387.1

Full Title Citation Front Review Clarabication Date Researce Sequences Attachments

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7. Document ID: US 6399332 B1

L11: Entry 7 of 18

· File: USPT

Jun 4, 2002

US-PAT-NO: 6399332

DOCUMENT-IDENTIFIER: US 6399332 B1

TITLE: Bacterial superantigen vaccines

DATE-ISSUED: June 4, 2002

INVENTOR-INFORMATION:

NAME

CITY

STATE ZIP CODE

COUNTRY

Ulrich; Robert G. Olson; Mark A. Frederick Gaithersburg MD MD

Bavari; Sina

Dillsburg

PA

Foll : Title | Citation | Front | Feview | Classification | trate | Feterance | Sequences | Attachineres |

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8. Document ID: US 6340461 B1

L11: Entry 8 of 18

File: USPT

Jan 22, 2002

US-PAT-NO: 6340461

DOCUMENT-IDENTIFIER: US 6340461 B1

TITLE: Superantigen based methods and compositions for treatment of diseases

DATE-ISSUED: January 22, 2002

INVENTOR-INFORMATION:

NAME

CITY

STATE ZIP CODE

COUNTRY

Terman; David Stephen

Pebble Beach

CA

93953

US-CL-CURRENT: 424/193.1; 424/192.1, 424/194.1, 424/277.1, 424/278.1, 424/280.1, 424/282.1, 435/68.1, 435/69.1, 435/69.3 , 435/69.7

Full : Title | Chatton | Front | Review | Classification | Date | Reterance | Sequences | Attachments |

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9. Document ID: US 6338845 B1

L11: Entry 9 of 18

File: USPT

Jan 15, 2002

US-PAT-NO: 6338845

DOCUMENT-IDENTIFIER: US 6338845 B1

TITLE: Tumor killing effects of enterotoxins, superantigens, and related compounds

DATE-ISSUED: January 15, 2002

INVENTOR-INFORMATION:

CITY

STATE

ZIP CODE

COUNTRY

Terman; David S.

Pebble Beach

CA

93953

US-CL-CURRENT: 424/93.1; 424/93.2, 424/93.21, 424/93.7, 424/93.71, 435/372, 435/372.1, 435/372.2, 435/372.3

10. Document ID: US 6251385 B1

L11: Entry 10 of 18

File: USPT

Jun 26, 2001

US-PAT-NO: 6251385

DOCUMENT-IDENTIFIER: US 6251385 B1

TITLE: Method of cancer treatment

DATE-ISSUED: June 26, 2001

INVENTOR-INFORMATION:

NAME

CITY

STATE ZIP CODE

COUNTRY

Terman; David S.

Pebble Beach CA

93953

US-CL-CURRENT: 424/93.7; 424/184.1, 424/236.1, 424/237.1, 424/277.1, 424/93.1, 424/93.2, $424/9\overline{3.71}$, $435/\overline{325}$

Full | Illie | Caution | Front | Review | Classicistion | Cute | Reference | Sequences | Attachments | 2000 | Draw Cero | Intogal

11. Document ID: US 6221351 B1

L11: Entry 11 of 18

File: USPT

Apr 24, 2001

US-PAT-NO: 6221351

DOCUMENT-IDENTIFIER: US 6221351 B1

TITLE: Tumor killing effects of enterotoxins, superantigens, and related compounds

DATE-ISSUED: April 24, 2001

INVENTOR-INFORMATION:

NAME

CITY

STATE ZIP CODE

COUNTRY

Terman; David S. Pebble Beach CA 93953

US-CL-CURRENT: 424/93.71; 424/93.1, 424/93.2, 424/93.21, 424/93.7, 435/69.3, 514/44, <u>530/395</u>

Fill Title Chatton Front Scotion Classification Date Reference Sequences Attachinants - John Draw Fuse I Image

12. Document ID: US 6126945 A

L11: Entry 12 of 18

File: USPT

Oct 3, 2000

US-PAT-NO: 6126945

DOCUMENT-IDENTIFIER: US 6126945 A

TITLE: Tumor killing effects of enterotoxins, superantigens, and related compounds

DATE-ISSUED: October 3, 2000

INVENTOR-INFORMATION:

NAME

CITY

STATE ZIP CODE COUNTRY .

Terman; David S. Stone; Jay L.

Aptos

Pebble Beach

CA CA

US-CL-CURRENT: 424/237.1; 424/236.1, 424/243.1, 424/244.1, 435/69.1, 435/69.3, 514/12, 514/8

Foil | Title | Cristian | Front | Front | Front | Classication | Classication | State | Reservation | Sequences | Attachments | Front | Front Uses | Broady

13. Document ID: US 6075119 A

L11: Entry 13 of 18

File: USPT

Jun 13, 2000

US-PAT-NO: 6075119

DOCUMENT-IDENTIFIER: US 6075119 A

TITLE: Peptides useful for reducing symptoms of toxic shock syndrome

DATE-ISSUED: June 13, 2000

INVENTOR-INFORMATION:

STATE ZIP CODE COUNTRY CITY

TN Bannan; Jason D. Thompson Station Zabriskie; John B. New York NY

Figs | Title | Caution | Front | Review | Classication | Date | Reference | Sequences | Attachments | PARC | Draw freto | Image |

14. Document ID: US 5872233 A

Feb 16, 1999 L11: Entry 14 of 18 File: USPT

US-PAT-NO: 5872233

DOCUMENT-IDENTIFIER: US 5872233 A

TITLE: Mycoplasma arthritidis T-cell mitogen

DATE-ISSUED: February 16, 1999

INVENTOR-INFORMATION:

Pole; Ann

· STATE ZIP CODE COUNTRY CITY NAME .

Cole; Barry C. UT Sandy

Salt Lake City Atkin; Curtis L. UT Oliphant; Arnold R. Johnston

Full | Title | Criation | Front | Review | Classication | Date | Reference | Sequences | Attachments |

US-CL-CURRENT: 536/23.7; 435/69.1, 436/86, 530/300, 530/324, 530/350, 536/22.1,

Salt Lake City UT

536/23.1, 536/25.3

L11: Entry 15 of 18 File: USPT Aug 18, 1998

KNOC - Evans Evans - Irosage

US-PAT-NO: 5795974

DOCUMENT-IDENTIFIER: US 5795974 A

TITLE: Mycoplasma arthritidis superantigen

15. Document ID: US 5795974 A

DATE-ISSUED: August 18, 1998

INVENTOR-INFORMATION:

CITY STATE ZIP CODE COUNTRY NAME

Cole; Barry C. Sandy UT Atkin; Curtis L. Holladay IIT -Knudtson; Kevin L. Salt Lake City UT

US-CL-CURRENT: 536/23.7; 435/5, 435/7.2

Full Title Caston Finnt Review Claredication Date Reference Sequences Attochnicate 1982 Prev Desc Image

16. Document ID: US 5728388 A

L11: Entry 16 of 18

File: USPT

Mar 17, 1998

US-PAT-NO: 5728388

DOCUMENT-IDENTIFIER: US 5728388 A

TITLE: Method of cancer treatment

DATE-ISSUED: March 17, 1998

INVENTOR-INFORMATION:

NAME CITY

STATE

ZIP CODE

Terman; David S.

Pebble Beach

CA

93953

US-CL-CURRENT: 424/237.1; 424/236.1

Full Title Castion Front : Feview Classrication Date Reservace Singlemons Educitiments - NINE Draw Derc Image

17. Document ID: US 5639869 A

L11: Entry 17 of 18

File: USPT

Jun 17, 1997

COUNTRY

US-PAT-NO: 5639869

DOCUMENT-IDENTIFIER: US 5639869 A

TITLE: Mycoplasma arthritidis T-cell mitogen

DATE-ISSUED: June 17, 1997

INVENTOR-INFORMATION:

NAME

CITY

STATE ZIP CODE COUNTRY

Cole; Barry C. Atkin; Curtis L. Sandy

UT

Oliphant; Arnold R.

UT

Johnston

Pole; Ann

Salt Lake City Salt Lake City

UT

US-CL-CURRENT: 536/23.7; 424/264.1, 530/326, 530/350, 530/825

Full | little | Citation | Front | Sevieur | Classification | Dato | Reference | Sequences | Attachments |

18. Document ID: US 6447777 B1 WO 9736614 A1 AU 9724293 A

L11: Entry 18 of 18

File: DWPI

Sep 10, 2002

DERWENT-ACC-NO: 1997-549326

DERWENT-WEEK: 200263

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TITLE: Use of crosslinked Staphylococcal protein A - for treating auto-immune diseases, transplant rejection neoplastic diseases or infectious disease such as HIV infection



INVENTOR: REISER, R F; TERMAN, D S

PRIORITY-DATA: 1996US-024802P (March 29, 1996), 1997US-0828951 (March 28, 1997)

PATENT-FAMILY:

PUB-NO	PUB-DATE	LANGUAGE	PAGES	MAIN-IPC
US 6447777 B1	September 10, 2002		000	A61K039/02
WO 9736614 A1	October 9, 1997	E	100	A61K039/09
AU 9724293 A	October 22, 1997		. 000	A61K039/09

 $\begin{array}{l} \text{INT-CL (IPC): } \underline{A61} \ \underline{K} \ \underline{38/00}; \ \underline{A61} \ \underline{K} \ \underline{39/02}; \ \underline{A61} \ \underline{K} \ \underline{39/04}; \ \underline{A61} \ \underline{K} \ \underline{39/05}; \ \underline{A61} \ \underline{K} \ \underline{A61} \ \underline{K} \ \underline{39/05}; \ \underline{A61} \ \underline{K} \ \underline{A61} \ \underline{A61} \ \underline{K} \ \underline{A61} \ \underline{A61$

Full Title Chatern Front Review Classification Date Retembre Seguences Attachments

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Term	Documents
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908470 seqs, 133250620 residues

Searched:

Scoring table:

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Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

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	2: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*	
	3: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1982.DAT:*	
	4: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1983.DAT:*	
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	13: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1992.DAT:	
	14: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1993.DAT:	•
	15: /SIDSZ/gcgdata/geneseq/geneseqp-embl/AA1994.DAT:	
	16: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1995.DAT:	
	17: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1996.DAT:	•
	18: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1997.DAT:	
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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20112101	72612161	AAW12148	AAW12147	AAW12150	AAW12146	AAW12154	AAW59780	AAW12097	ABB79508	AAY70109	ID	
Streptococcus byog					Streptococcus pyog	Streptococcus pyog	Amino acid sequenc	Streptococcus pyog		Streptococcal pyro	Description	

45	44	4	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11
544	544	544	544	544	545	545	546	547	549	553	553	558	558.5	561	561	562	563	563	565.5	567.5	574	575	576	588	1164	1164	1164	1170	1286	1288	1288.5	1293	1298	1298
41.1	41.1	41.1	41.1	41.1	41.2	41.2	41.3	41.4	41.5	41.8	41.8	42.2	42.2	42.4	42.4	42.5	42.6	42.6	42.8	42.9	43.4		43.6		88.0		88.0	88.5		97.4		97.8		
239	239	239	239	239	238	238	238	239	265	266	266	239	266	239	239	239	240	239	266	266	239	266	239	255	221	221	221	221	251	251	250	251	251	251
23	22	20	14	12	22	14	23	20	21	23	21	21	23	14	12	23	21	23	21	23	22	21	19	18	23	14	12	22	19	19	18	18	18	18
ABB76238	AAB67342	AAY06251	AAR45015	AAR13207	AAB67343	AAR45016	ABB76239	AAY06254	AAY70104	ABB79507 ·	AAY70108	AAY70106	ABB79504	AAR45014	AAR13206	ABB76237	AAY54465	ABB79505	AAY54464	ABB79503	AAB67341	AAY92319	AAW64647	AAW06737	ABB76240	AAR45017	AAR13209	AAB67344	AAW59781	AAW59798 .	AAW12145	AAW12149	AAW12153	AAW12152
Staphylococcus aur	Staphylococcus aur	Staphylococcal gro	Staphylococcal ent	Staphylococcal ent	Staphylococcus aur	Staphylococcal ent	-	_	•	•	Staphylococcal ent	^	Staphylococcal ent			Staphylococcus aur	Mutant Staphylococ	Staphylococcal ent	Amino acid sequenc	Staphylococcal ent	Staphylococcus aur	Plant-optimized mu	Synthetic SEB prot						Amino acid sequenc	Amino acid sequenc	SnS	Streptococcus pyog		Streptococcus pyog

ALIGNMENTS

RESULT 1 AAY70109 D AAY70109 standard; Protein; 251 AA.

AAY70109;

Streptococcal pyrogenic exotoxin A (SPE-A)

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diagnosis; treatment; superantigen-associated bacterial infection.	cytostatic; antibody; staphylococcal/streptococcal toxin; toxoid; SPEA42;	antibacterial; vaccine; MHC class II receptor; T-cell antigen receptor;	Superantigen toxin; SAg; Streptococcal pyrogenic exotoxin A; SPE-A;
reatment	antibody	1; vacci	toxin;
; sup	; sta	ne; x	SAg;
erantigen-as	phylococcal/	HC class II	Streptococca
sociated ba	streptococc	receptor; T	11 pyrogenic
cterial	al toxi	-cell a	exotox
infec	n; tox	ntigen	in A;
tion.	oid;	rece	SPE-A
	SPEA42	ptor;	•

Streptococcus sp.

WO200009154-A1.

²⁴⁻FEB-2000.

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⁰⁵⁻JUN-2000 (first entry)

⁽REED-) REED ARMY INST RES WALTER.

Ulrich RG, Olson MA, Bavari S;

WPI; 2000-224177/19. N-PSDB; AAZ51112.

Nucleic acid encoding superantigen toxin useful as a vaccine and for

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          exorbxin A (SPE-A) a bacterial superantigen toxin (Shg), used for the formulation of SPE-A vaccine SPEAA. The coding region of this Shg toxin is altered by site directed mutagenesis, introducing 142R mutation, that results in disruption of binding of the toxin to both the HIC class II or T-cell antigen receptor. SPE-A has antibacterial and cytostatic activity. This sequence is useful for the production of SPE-A vaccines and specific antibodies. This vaccine overcomes the disadvantages of the chemically inactivated toxoids and is designed to protect individuals against one or several related staphylococcal and streptococcal toxins. It is used for the diagonals and treatment or amelioration of
                                                                                                                                                       01-SEP-1998;
                                                                                                                                                                                                                               US6399332-BI
                                                                                                                                                                                                                                                                                                                                           Exotoxin A;
       WPI; 2002-546281/58
                                                                            (USSA) US
                                                                                                                   25-JUN-1997;
                                                                                                                                                                                           04-JUN-2002
                                                                                                                                                                                                                                                                   Synthetic.
                                                                                                                                                                                                                                                                                     Streptococcus
                                                                                                                                                                                                                                                                                                                         attenuation;
                                                                                                                                                                                                                                                                                                                                                                         Streptococcal pyrogenic exotoxin A vaccine SPEa42.
                                                                                                                                                                                                                                                                                                                                                                                                                  23-SEP-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABB79508;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABB79508 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
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                                           RG,
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                                                                            SEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           251 AA;
                                           Olson
                                                                                                                                                                                                                                                                                                                                        SPEa; SPEa42; superantigen; antigen; toxin; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                      mutant; mutein
                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                  pyogenes
                                                                            OF ARMY
                                                                                                                97US-0882431
                                                                                                                                                       98US-0144776
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                                           Bavari
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Pred. No. 4
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SAg), used
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            co pyogenes vaccine SPBA42. The vaccine differs from the native SPBA content by substitution of the Accidence of the National State 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 251;
                                                                                                         Streptococcal; toxin A; SPE-A; non-lethal; mutant; production; vaccine; protection; treatment; cancer; neutralising antibody; streptococcal toxic shock syndrome; STSS; symptom; amelioratio fever; hypotension; group A streptococcal ioxic chor; myosilatis; fascitis; liver damage; T cell; hymphoma; overlan; uterine;
                 Peptide
                                                                                                                                                                                                                                                                04-NOV-1997
                                                                       Streptococcus
                                                                                                                                                                                                                       Streptococcus
                                                                                                                                                                                                                                                                                                                                     AAW12097
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel isolated and purified superantigen toxin DNA fragment which has been genetically altered, useful for producing vaccine for treatment of superantigen toxin-associated bacterial diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; ABN84229
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity 100
51; Conservative
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                                                                                                                                                                                                                                                                                                                                     standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    TSQIEVYLTTK 251
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                                                                                                                                                                                                                                                                                                                                                                                                                               TSQIEVYLTTK 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KYLTDNKQLYTNGPSKYETGYIKFIPKNKESFWFDFFPEPEFTQSKYLMIYKDNETLDSN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KYLTDNKQLYTNGPSKYETGYIKFIPKNKESFWFDFFPEPEFTQSKYLMIYKDNETLDSN 240
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                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                       pyogenes Streptococcal toxin
                                                                       pyogenes
/label= sig_peptide
                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%;
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Pred. No. 4.5e-111;
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                                                                                                         symptom; amelioration;
infection; myositis;
ovarian; uterine.
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RESULT 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence is Streptococcus pyogenes Streptococcal toxin a (SPE-A) comprising at least 1 amino SPE-A, comprising at least 1 amino special matent SPE-A, comprising at least 1 amino special control of the metal of the metal special control of the special control of the metal special control of the special contro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Sir
Matches 249;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Pages 77-79; 102pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mutant SPE-A toxin with at least one amino acid change is substantially non-lethal - used in vaccine composition fi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (MINU ) UNIV MINNESOTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                   12-OCT-1998
                                                                                    AAW59780 standard; Protein;
                                                  AAW59780;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
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                                                                                                                                                                                        TSQIEVYLTTK 251
                                                                                                                                                                                                                                                                        KYLTDNKQLYINGPSKYETGYIKFIPKNKESFWFDFFPEFETQSKYLMIYKDNETLDSN 240
                                                                                                                                                                                                                                                                                                            ENAERSACIYGGVTNHEGNHLEIPKKIVVKVSIDGIQSLSFDIETNKKMVTAQELDYKVR
                                                                                                                                                                                                                                                                                                                            ENAERSACIYGGYTNHEGNHLEIPKKIYVKVSIDGIQSLSFDIETNKKMYTAQELDYKVR
                                                                                                                                                                                                                                        TSQIEVYLTTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      251 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Roggiani M,
                   (first entry)
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/label- mat_peptide
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Pred. No. 8.3e-110;
0; Mismatches 2;
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shock syndrome
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AAW12154
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This is the amino acid sequence of the Streptococcus pyogens excitain A (SPE-A toxin). The novel mutant Streptococcal SPE-A toxin has at least least cachange and is nonlethal compared with a protein to wild type SPE-A toxin. The mutant SPE-A toxins are nontoxic and can produce antibodies that neutralise wild type SPE-A toxin activity. The toxins can be used in vaccines and therapeutics to generate a protective immune response against streptococcal infection. They can be used to protect against the development of streptococcal toxic shock syndrome (STSS). In addition, the toxins can be used for treating animals with symptoms of the toxins can be used for treating animals with symptoms of the treatment of cancer. In particular they can be used for treating T cell lymphomas, and ovarian and uterine cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Streptococcus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New mutant Streptococcal SPE-A toxins - or treatment of streptococcal infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ohlendorf D,
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                          AAW12154 standard; Protein; 251
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                                                                                                                                                                                                                                                                                                                   61 THENVKSVDQLLSHHLIYNVSGPNYDKLKTELKNQEMATLFKDKNVDIYGVEYYHLCYLC
                                                                                                                                                                                                                                                                                                                                      61 THENVKSVDQLRSHDLIYNVSGPNYDKLKTELKNQEMATLFKDKNVDIYGVEYYHLCYLC
                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                TSQIEVYLTTK 251
                                                                                                              TSQIEVYLTTK 251
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            0
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 1308; DB 19;
Pred. No. 8.3e*110;
0; Mismatches 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     useful for, e.g. prevention or toxic shock syndrome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Stoehr
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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                                                                                                                                                                                                                               The present sequence is a non-lethal Streptococcus pyogenes Streptococcal toxin A (SPE-A) mutant, which can be used to produce vaccines to protect animals against wild type SPE-A and to treat concer and streptococcal toxic shock syndrome (STSS). The mutant SPE-A concertaints are streptococcal through the syndrome (STSS). The mutant can be used to ameliorate STSS symptoms, e.g. fever, hypotension, and the streptococcal infection, myositis, fascitis and liver damage. The neutralising Ab is preferably administered in the conjunction with antiblotic therapy. The mutant SPE-A is especially useful for treating T cell lymphomas, and overian and tetrine cancer. It is thought that mutant SPE-A can be selectively toxic to T cell lymphoma colls.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                       Query Match
Best Local
                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mutant SPE-A toxin with at least one maino acid change is substantially non-lethal - used in vectine composition for treatment of cancer and streptococcal toxic shock syndrome etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 4; Page -; 102pp; English.
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            121
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                                                                                                                                                                     Similarity
ENAERSACIYGGVTNHEGNHLEIPKKIVVKVSIDGIQSLSEDIETNKKMVTAQELDYKVR 180
                            THENVKSYDQLLSHHLIYNVSGPNYDKLKTELKNQEMATLFKDKNVDIYGVEYYHLCYLC
                                             THENVKSVDQLRSHDLIYNVSGPNYDKLKTELKNQEWATLFKDKNVDIYGVEYYHLCYLC
                                                                                   MENNKKYLKKMYFFYLYTFLGLTISQEYFAQQDPDPSQLHRSSLYKNIQNIYFLYEGDPY
                                                                                                      MENNKKYLKKAYFFYLYTFLGLTISGEYFAQQDPDPSQLHRSSLYKNLQNIYFLYBGDPY
                                                                                                                                                                                                                251
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     95US-0480261.
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/label= sig_peptide
31..251
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                                                                                                                                                                   98.7%;
                                                                                                                                                 Score 1305; DB 1B;
pred. No. 1.5e-109;
1; Mismatches 2;
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The present sequence is a non-lethal Streptococcus pyogenes

Streptococcal toxin A (SPE-A) mutant, which can be used to produce
vaccines to protect animals against which can be used to produce
vaccines to protect animals against which can be used to treat
cancer and streptococcal toxic shock syndrome (STSS). The mutant
SPE-A causes neutralising antibodies (Ab) to be produced, which
may be used to ameliorate STSS symptoms, e.g. fever, hypotension,
yroup A streptococcal infection, myositis, fascitis and liver
damage. The neutralising Ab is preferrably administered in
conjunction with antiblotic therapy. The mutant SPE-A is
especially useful for treating T cell lymphomas, and ovarian and
toxic toxic to T cell lymphoma cells.

M.B. Sequence not given in the specification, but constructed
using the wild type SPE-A sequence given on pages 77-79.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mutant SPE-A toxin with at least one amino acid change is
substantially non-lethal - used in weache composition for
treatment of cancer and streptococcal toxic shock syndrome etc.
                                                                                                                                                                                                                                                                                                                                                                                                                             Claim
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
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187
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RESULT 7
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Streptococcus pyogenes Streptococcal toxin A mutant Lys16Asn.
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             Mutant SPE-A toxin with at least one amino acid change is substantially non-lethal used in vaccine composition for treatment of cancer and streptococcal toxic shock syndrome etc.
                                                                                                                                                                                                                                                                                                                                                                               Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      vaccine; protection; treatment; cancer; neutralising antibody; streptococcal toxic shock syndrome; STSS; symptom; amelioration; fever; hypotension; proup A streptococcal infection; myositis; fascitis; liver damage; T cell; lymphoma; ovarian; uterine.
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                                                                                                                                                                                                         07-JUN-1995;
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Synthetic.
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Pred. No. 1.9e-109;
1; Mismatches 2;
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Best Local s
Matches 248
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No. Sequence not given in the specification, but constructed toxic to Tocal lymphoma cells.
                                                                                                                                              Key
Peptide
                                                                       Misc-difference
                                                                                                                                                                                                      Streptococcus
Synthetic.
                                                                                                                                                                                                                                                           vaccine; protection; treatment; cancer; neutralising antibody; streptococcal toxic shock syndrome; STSS; symptom; amelioration; fever; hypotension; group A streptococcal infection; myositis; fascitis; liver damage; T cell; lymphoma; ovarian; uterine.
                                                                                                                                                                                                                                                                                                                                     Streptococcal; toxin A; SPE-A; non-lethal; mutant; production;
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               W09640930-A1
                                                                                                            Peptide
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31..251
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Streptococcal; toxin A; SPE-A; non-lethal; mutant; production; vaccine; protection; treatment; cancer; neutralising antibody; streptococcal toxic shock syndrome; STSS; symptom; ameliorated
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                                                                            Streptococcus pyogenes Streptococcal toxin A mutant N20D/K157E
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Sequence not given in the specification, but constructed with stipe SPEA sequence given on pages 77-79.
                                                                                                                                                                                                                                                                                Mutant SPE-A toxin with at least substantially non-lethal - used
Sequence
                                                                                                                                                                                                                                         Claim 5; Page -; 102pp; English.
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fascitis; liver damage; T cell; lymphoma; ovarian; uterine.
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                                                                                                                                                                                                                                                                 coxin with at least one amino acid change is y non-lethal - used in vaccine composition for cancer and streptococcal toxic shock syndrome etc.
                                                                                                                                                                                                                                                                                                                                                                                    MINNESOTA
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187
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Query Match
Best Local
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                                    181
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247; Conserv
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                                                                                                                                                                                                                               1 MENNKKVLKKMVFFVLVTFLGLTISQEVFAQQDPDPSQLHRSSLVKNLQNIYFLYEGDPV
KYLTONGOLYTNGPSKYETGYIKFIPKNKESFWEDFPBEBETGSKYLMIYKONETLOSN 240
KYLTONGOLYTNGPSKYETGYIKFIPKNKESFWEDFPBEBETGSKYLMIYKONETLOSN 240
KYLTONEGLYTNGPSKYETGYIKFIPKNKESFWEDFPBEPBETGSKYLMIYKONETLOSN 240
                                                                   THENVKSVDQLRSHDLIYNVSGPNYDKLKTELKNQEMATLFKDKNVDIYGVEYYHLCYLC 120
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                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                98.3%;
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                                                                                                                                                                                                                                                                             Score 1299; DB 18;
Pred. No. 5.4e-109;
2; Mismatches 2;
                                                                                                                                                                                                                                                                               Indels
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RESULT 10
AAW12151
ID AAW12151
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                                                                                                                                                            C The present sequence is a non-lethal Streptococcus pyogeness Streptococcal toxin A (SPEA) mutant, which can be used to produce vaccines to protect animals against wild type SPEA and to treat cancer and streptococcal toxic shock syndrome (STSS). The mutant SPEA causes neutralising antibodies (Ab) to be produced, which may be used to ameliorate STSS symptoms, e.g. fever, hypotension, croup a streptococcal infection, myositis, facitis and liver damage. The neutralising ab is preferably administered in conjunction with antiblocic therapy. The mutant SPEA is sepcially useful for treating To cell lymphomas, and overian and tetrine cancer. It is thought that mutant SPEA can be selectively toxic to Total lymphoma cells.

20 M.B. Sequence not given in the specification, but constructed withing the wild type SPEA sequence given on pages 77-79.
           Query Match
Best Local Similarity
Matches 248; Conserv
                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mutant SPE-A toxin with at least
substantially non-lethal - used
treatment of cancer and streptoco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Streptococcal; toxin A; SPF-A; non-lethal; mutant; production; vaccine; protection; treatment; cancer; neutralising antibody; supplemental toxic shock syndrome; STSS; symptom; amelioration; fever; hypotension; group A streptococcol infection; myssitis; fascitis; liver damage; T cell; lymphoma; vorzin; uterine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 4; Page -; 102pp; English.
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               Conservative
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       Score 1298; DB 18;
Pred. No. 6.6e-109;
0; Mismatches 3;
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07-JUN-1995;

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Roggiani M,

Schlievert PM,

The present sequence is a non-lethal Streptococcus pyogenes Streptococcal toxin A (SPE-A) mutant, which can be used to produce vaccines to protect unimals against wild type SPE-A and to treat cancer and streptococcal toxic shock syndrome (STSS). The mutant

neutralising

antibodies

<u>8</u>

to be

produced,

which

Mutant SPE-A toxin with at least one amino acid change is substantially non-lethal - used in vaccine composition for treatment of cancer and streptococcal toxic shock syndrome

etc

Page

-; 102pp;

English.

WPI; 1997-099936/09 Ohlendorf D,

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RESULT 11
AAW12152
ID AAW12
                                                                                                                                                                                                                                                                                                                      Streptococcal; toxin A, SBE-A, non-lethal; mutant; production; vaccine; protection; transment; cancer; neutralising antibody; streptococcal toxic shock syndrome; STSS; symptom, amelioration; fever; hypoten sion; group A streptococcal infection; myositis; fascitis; liver damage; T cell; lymphoma; ovarian; uterine.
07-JUN-1996;
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96WO-US10252
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31..251
                                                                                                          /note= "wild type Cys
                                                                                                                                                  /label- mat_peptide
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                                                                                                                                                                                    sig_peptide
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                                                                                                               Ser*
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Matches 248
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MENNKKYLKKMVFFVLVTFLGLTISQEVFAQQDPDPSQLHRSSLVKNLQNIYFLYEGDPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TSQIEVYLTTK 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MENNKKYLKKMYFFYLYTFLGLTISQEVFAQQDPDPSQLHRSSLYKNLQNIYFLYEGDPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TSQIEVYLTTK 25:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ENAERSASIYGGVTNHEGNHLEIPKKIVVKVSIDGIQSLSFDIETNKKMVTAQELDYKVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98.2%;
nilarity 98.8%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  251
                                                                                                                                                                                                                                                                                                                                                                                                                                 pyogenes
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                                               9505-0480261
                                                                                            96WO-US10252
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120
                                                                                                                                                                                                                                                                                                                    /label sig_peptide
                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   entry)
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                                                                                                                                                                                                                           wild type Cys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               251
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 1298; I
Pred. No. 6.6e
0; Mismatches
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6.6e-109;
les 3;
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                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local S
Matches 248
                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence is a non-lethal Streptococcus pyogenes streptococcal toxin A (SBEA) mutant, which can be used to produce vaccines to protect animals against wild type SBEA and to treat cancer and streptococcal toxic shock syndrame (SPES). The mutant SBEA causes neutralising antibodies (Ab) to be produced, which may be used to amellorate SPES symptoms e 9, fever, hypotension, group A streptococcal infection myositis, fascitis and liver cancer and the neutralising Ab is preferably administered in conjunction with antibiotic therapy. The mutant SBEA and overlan and utile cancer. It is thought that mutant SBEA can be selectively toxic or Teell lymphoma call implomes, and overlan and streptocal toxic or Teell lymphoma to the specification, but constructed the selectively that SBEA can be selectively that SBEA can be selectively that several cancer are a specially cancer and the selectively cancer and selective cancer and selecti
                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 4; Page -; 102pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             treatment of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mutant SPE-A toxin with a substantially non-lethal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ohlendorf D,
                                                                                                                                                                                                                                248;
                                                                                                                                                                                                                                                                                                                                                                                                    the wild type SPE-A sequence given
                                                        61
                                                                                                            Similarity
THENVKSVDQLLSHHLIYNVSGPNYDKLKTELKNQEMATLFKDKNVDIYGVEYYHLCYLS
                                    THENVKSVDQLRSHDLIYNVSGPNYDKLKTELKNQEMATLFKDKNVDIYGVEYYHLCYLC
                                                                                                                                                                                                                                                                                                                                                251 AA;
                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cancer and streptococcal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Roggiani
                                                                                                                                                                                                                                                        98.2%;
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                                                                                                                                                                                                                                                        Score 1298;
Pred. No. 6.
                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     one amino acid change is
in vaccine composition for
occal toxic shock syndrome etc.
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                                                                                                                                                                                                                                                                                                                                                                                            tion, but constructed on pages 77-79.
                                                                                                                                                                                                                                                            .6e-109;
                                                                                                                                                                                                                                                                                        DB
                                                                                                                                                                                                                                                                                        Length
                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                            251;
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                                                                                                                                                                                                                                Gaps
                                                        120
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RESULT 13
AAW12149
ID AAW13
                                                              streptococcal toxic shock syndrome; STSS; symptom; amelioration; fever; hypotension; group A streptococcal infection; myositis; fascitis; liver damage; T cell; lymphoma; ovarian; uterine.
Streptococcus
Synthetic.
                                                                                                                                                      Streptococcal; toxin A; SPE-A; non-lethal; mutant; production;
                                                                                                                                                                                                     Streptococcus
                                                                                                                                                                                                                                                 04-NOV-1997
                                                                                                                                                                                                                                                                                                AAW12149;
                                                                                                                                   vaccine; protection; treatment; cancer; neutralising
                                                                                                                                                                                                                                                                                                                                            AAW12149
                                                                                                                                                                                                                                                                                                                                            standard;
                                                                                                                                                                                                                                                 (first entry)
                     pyogenes
                                                                                                                                                                                                     pyogenes Streptococcal toxin
                                                                                                                                                                                                                                                                                                                                            Protein;
                                                                                                                                                                                                                                                                                                                                            251
                                                                                                                                                                                                        A mutant N20D/C98S
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antibody;

FXXS XXX XXX XXX XXX

Key

Location/Qualifiers

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241 241 181 181 121 121

TSQIEVYLTTK

.251 251

TSQIEVYLTTK

KYLTDNKQLYTNGPSKYETGYIKFIPKNKESFWFDFFPEPEFTQSKYLMIYKDNETLDSN

ENAERSACIYGGVTNHEGNHLEIPKKIVVKVSIDGIQSLSFDIETNKKMVTAQELDYKVR ENAERSACIYGGVTNHEGNHLEIPKKIYVKVSIDGIQSLSFDIETNKKMVTAQELDYKVR

KYLTDNKQLYTNGPSKYETGYIKFIPKNKESFWFDFFPEPEFTQSKYLMIYKDNETLDSN

240 240 180 180 120

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RESULT 14
AAW12145
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C The present sequence is a non-lethal Streptococcus progeness treptococcal toxin A (SPEA) mutant, which can be used to produce vaccines to protect animals against wild type SPEA and to treat a profession of the sequence o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
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substantially non-lethal - used in vaccine composition for
treatment of cancer and streptococcal toxic shock syndrome etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ohlendorf D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 07-JUN-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 5; Page -; 102pp; English.
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les 247; Conserv
                                                                              241
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                                                                                                                                                                                                                                                                                                                                   THENVKSVDQLRSHDLIYNVSGPNYDKLKTELKNQEMATLFKDKNVDIYGVEYYHLCYLC
                                                                                                                                                                             KYLTDNKQLYTNGPSKYETGYIKFIPKNKESFWFDFFPEPEFTQSKYLMIYKDNETLDSN
                                                                                                                                                                                                                                    ENAERSASIYGGVTNHEGNHLEIPKKIVVKVSIDGIQSLSEDIETNKKAVTAQELDYKVR
                                                                                                                                                                                                                                                       ENAERSACIYGGVTNHEGNHLEIPKKIVVKVSIDGIQSLSFDIETNKKMVTAQELDYKVR
                                                                                                                                                                                                                                                                                                                THENVKSVDQLLSHHLIYNVSGPNYDKLKTELKNQEMATLFKDKNVDIYGVEYYHLCYLC
                                                                              TSQIEVYLTTK 251
                                                                                                                    TSQIEVYLTTK 251
                                                                                                                                                          KYLTONKQLYTNGPSKYETGYIKFIPKNKESFWFDFFPEPEFTQSKYLMIYKDNETLDSN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       251 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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128
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50
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/label= sig_peptide
31..251
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           97.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "wild type Asn replaced by Asp"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 1293; DB 18;
Pred. No. 1.9e-108;
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Matches
                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                   damage. The neutralising Ab is preferably administered in conjunction with antibiotic therapy. The mutant SPE-A is especially useful for treating T cell lymphomas, and ovarian and uterine cancer. It is thought that mutant SPE-A can be selective toxic to T cell lymphoma cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                               Streptococcal toxin A (SPE-A) mutant, which can be used to produce vaccines to protect animals against wild type SPE-A and to treat cancer and streptococcal toxic shock syndrome (STSS). The mutant SPE-A causes neutralising antibodies (Ab) to be produced, which may be used to ameliorate STSS symptoms, e.g. fever, hypotension, group A streptococcal infection, myositis, fascitis and liver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    vaccine; protection; treatment; cancer; neutralising antibody; streptococcal toxic shock syndrome; STSS; symptom; amelioration; fever; hypotension; oroup A streptococcal infection; myositls; fascitis; liver damage; T cell; lymphoma; ovarian; uterine.
                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                             N.B. Sequence not given in the specification, but constructed using the wild type SPE-A sequence given on pages 77-79.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mutant SPE-A toxin with at least one amino acid change is substantially non-lethal - used in waccine composition for treatment of cancer and streptococcal toxic shock syndrome etc.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 5; Page -; 102pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI;
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                                                                                                                                                                                                                   Poca I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1997-099936/09
121 ENAERSACIYGGVTNHEGNHLEIPKKIVVKVSIDGIQSLSFDIETNKKMVTAQELDYKVR 180
                                      61
                                                                            61
                                                                                                                                                                                                248;
                                                                                                                                                                                                                   Similarity
                                   THENVKSVDQLIASHILIYNVSGPNYDKLKTELKNQEMATLFKDKNVDIYGVEYYHLCYLC
THENVKSVDQLIASHILIYNVSGPNYDKLKTELKNQEMATLFKDKNVDIYGVEYYHLCYLC
THENVKSVDQLIASHILIYNVSGPNYDKLKTELKNQEMATLFKDKNVDIYGVEYYHLCYLC
                                                                                                                  MENNKKYLKKWYFFYLYTFLGLTISQEVFAQODDDSQLHRSSLYKNLONIYFLYEGDPV
MENNKKYLKKWYFFYLYTFLGLTISQEVFAQODDDSQLHRSSLYKNLONIYFLYEGDPV
MENNKYLKKWYFFYLYTFLGLTISQEVFAQODDDSQLHRSSLYKNLONIYFLYEGDPV
                                                                                                                                                                                                                                                                            250 AA;
                                                                                                                                                                                                Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 toxin A; SPE-A; non-lethal; mutant;
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                                                                                                                                                                                                                 98.8%;
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                                                                                                                                                                                                                 Pred. No. 4.7e-108;
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                                                                                                                                                                                                Mismatches
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                                  produce artibodies that neutralise wild type SPEA toxin activity. The toxins can be used in vaccines and therapeutics to generate a protective immune response against streptococcal infection. They can be used protect against the development of streptococcal toxic shock syndrome (SPSS). In addition, the toxins can be used for treating animals with symptoms of streptococcal infection or SPSS and in methods for stimulating Teal proliferation and in the treatment of cancer. In particular they can be used for treating Teal Tymphomas, and ovarian
                                                                                                                                                This is the amino acid sequence of the mutant Streptococcus pyogenes exotoxin A (SPE-A toxin). The novel mutant Streptococcal SPE-A toxin has at least 1 as change and is nonlethal compared with a protein to wild type SPE-A toxin. The mutant SPE-A toxins are nontoxic and can
                                                                                                                                                                                                                                                New mutant Streptococcal SPE-A toxins - useful for, e.g. prevention or treatment of streptococcal infection or toxic shock syndrome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SPP-A toxin; nonlethal; mutant; Streptococcus yyogenes exotoxin A; wild type; nontoxic; antibody; vaccine; immunity; overian cancer; streptococcal toxic shock syndrome; STSS; T cell lymphoma;
                                                                                                                                                                                                                       Claim 4; Page -; 95pp; English.
                                                                                                                                                                                                                                                                                            WPI; 1998-333330/29.
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                                                                                                                                                                                                                                                                                                                                                                            06-DEC-1996;
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                              nd uterine cancer.
             sequence was not present in
information given
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "Optionally Glu or Asp"
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             specification but was created
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Best Local
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                                                                                                                                                                                                                                                               Similarity
TSQIEVYLTTK
                      TSQIEVYLTTK 251
                                                                                                           ENAERSACIYGGVTNHEGNHLEIPKKIVVKVSIDGIQSLSFDIETNKKNVTAQELDYKVR 180
                                                                                                                                                            THENVKSVDQLRSHDLIYNVSGPNYDKLKTELKNQEMATLFKDKNVDIYGVEYYHLCYLC
                                                                                                                                                                                                              MENNKKVLKKMVFFVLVTFLGLTISQEVFAQQDPDPSQLHRSSLVKNLQNIYFLYEGDPV
                                              KYLTDNKQLYTNGPSKYETGYIKFIPKNKESFWFDFFPEPEFTQSKYLMIYKDNETLDSN
                                                           KYLTDNKQLYTNGPSKYETGYIKFIPKNKESFWFDFFPEPEFTQSKYLMIYKDNETLDSN
                                                                                               ENAERSACIYGGVTNHEGNHLEIPKKIVVKVSIDGIXSLSFDIETNKKMVTAQELDYKVR
                                                                                                                                                THENVKSVDQLLSHHLIYNVSGPNYDKLKTELKNQEMXTLFKDKNVDIYGVEYYHLCYLC
                                                                                                                                                                                              MENNKKYLKKMYFFYLYTFXGLTISQEYFAQQDPDPSQLHRSSLXKNLQNIYFLYEGDPV
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251
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Pred. No. 5.3e-108;
0; Mismatches 6;
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Search completed: June 23, 2003, Job time: 38.6551 secs 16:12:24

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein protein search, using sw model

June 23, 2003, 16:06:15; Search time 68.3449 Seconds

Run on:

(without alignments)
912.449 Million cell updates/sec

Title: Perfect score: US-10-002-784A-27 2500

Sequence: MQQDPDPSQLHRSSLVKNLQ.....ALGTGGGAGGFNGYQSAVVG 468

Scoring table: Gapop 10.0 , Gapext 0.5 BLOSUM62

Searched:

Total number of hits satisfying chosen parameters:

908470 seqs, 133250620 residues

908470

Maximum DB Minimum DB seq length: 0 seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database A_Geneseq_101002:* 1: /SIDS2/gcqdata/

/SIDS2/gcqdata/geneseq/geneseqp-embl/Ah1980.DAT:
/SIDS2/gcqdata/geneseq/geneseqp-embl/Ah1980.DAT:
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SIDS2/gogdata/genesety-genesetp-emb1/AA1986_DAT:

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result

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1123	1112	1129	1136	1136	1195.5	1323.5	1327.5	1327.5	1327.5	Score
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stapnyrococcar ent	Streptococcar pyro	Streptococcus pyro	Streptococcal pyro		Streptococcus pyog	Streptococcus poly	S. pyogenes cystei	S. pyogenes speB g	Streptococcus pyog	Description

Staphylococcal Staphylococcal Staphylococcus Staphylococcus Staphylococcus Staphylococcus Staphylococcus	AAY06254 AAY06254 ABB76239 AAR45016 AAB67343	21 23 23 23	238 238 238 8	00000	513.5 513 513 510 510
	AAR45014 AAR45014 ABB76237 AAY70106 ABB79504 AAY70108 ABB79507	14 23 23 23	2232233 23393 23393	000++++	114 225 7 8 8
	AAW64647 AAB67341 AAW66737 AAY92319 ABB79503 ABB79505 AAY54465 AAY54464	19 18 23 23 21	22222222222222222222222222222222222222	21.6 21.6 21.6 21.2	222222
	AAW12151 AAW12152 AAW12153 AAW12149 AAW12149 AAW59781 AAW59798	19 18 18 19	251 251 251 251 251		
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ALIGNMENTS

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AAW07898 standard; Protein; 398 AA.

AAW07898;

22-JUL-1997 (first entry)

Streptococcus pyogenes clone speB7 pre-pro cysteine protease.

Pre-pro; cysteine; protease; inhibition; neoplastic; proliferation;

cell; human; treatment; carcinoma; sarcoma; melanoma; lymphoma; leukaemia; leukemia; blood; lung; mammary gland; prostate; lutestine; stomach; llver; heart; skin; pancreas; brain tissue; wound covering; prevention; metastasis; identification; speB7.

Streptococcus pyogenes.

Key Location/Qualifiers

Domain Misc-difference /note= "corresponding codon TAG"
333...338

/label= nucleotide_binding_domain

W09634941-A1

07-NOV-1996

30-APR-1996; 96WO-US05997

(BAYU) BAYLOR COLLEGE MEDICINE.

01-MAY-1995;

95US-0432692.

(TEXA) UNIV TEXAS

SYSTEM

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Best Local :
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Immunogenic peptide; speB gene; extracellular protease; production; antibody; vaccine; diagnosis; detection; Streptococcus infection; group A; prevention; treatment; pharyngitis; tonsillitis; skin infection; acute rheumatic fever; scarlet fever; probe; post-streptococcal glamerilonephritis; sepsis; meningitis; erysipelis; cellulitis; fasciitis; toxic shock like syndrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      wound covering, and can also be used to prevent metastasis or identify susceptible neoplastic cells.

K1735 and CM519 melanoma cells were injected s.c. into nu/nu mice, optionally followed by i.p. injection of CP (100 microg, 24 hours later). The mice were checked twice weekly for tunour growth for 12 weeks, to give results that showed that treatment with CP completely protected atthmic mice against transplanted K1735 melanoma growth, and protected 60% of the mice from developing
                                                                                                                                                                                                       AAR95856 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence is the Streptococcus pyogenes close speB7 pre-pro cysteline protesses (CP), which can be used to inhibit neoplastic cell proliferation, especially in a human, useful in t trainment of neoplastic conditions especially are human, seeful in treatment of neoplastic conditions originating from blood, lung meanance, lymphomas and leakemias originating from blood, lung meanance; lymphomas and leakemias originating from the conditions are proceed or brain tissue, the Crisspecially associated with a penciess or brain tissue, the Criss specially associated with a
                                                                                                                                                 30-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Use of extracellular Streptococcal cysteine protesse enzyme -
inhibiting the proliferation of neoplastic cells, e.g. for tre
carcinoma, lymphoma or leukaemia.
                                                                                                               pyogenes
                                                                                                                                                                                                                                                                                              354
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                                                                                                                                                                                                                                                                                                                                                      AISTRQYNWNNILPTYSGRESNVQKMAISELMADVGISVDMDYGPSSGSAGSSRVQRALK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EKYKPGEQSFYGQHAATGCYATATAQIMKYHNYPNKGLKDYTYTLSSNNPYFNHPKNLFA
                                                                                                                                                                                                                                                                                            HVNWGWGGVSDGFFRLDALNPSALGTGGGAGGFNGYQSAVVG
                                                                                                                                                                                                                                                                                                                                                                                     ENFGYNOSVHQINRSDFS-QDWEAQIDKELSQNQPVYYQG-GKVGGHAFVIDGADGRNFY
                                                                                                                                                                                                                                                                                                                                                                                                                     AISTROYNWNNILPTYSGRESNVOKMAISELMADVGISVDMDYGPSSGSAGSSRVORALK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EKYKPGEQSFYGQHAATGCVATATAQIMKYHNYPNKGLKDYTYTLSSNNPYFNHPKNLFA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             398 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pages 59-61; 99pp; English.
                                                                                                                                             (first entry)
                                                                                                             gene encoded extracellular protease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              53.1%;
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5; Mismatches
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Best Local
                                                                                                                                                                                                                                                                                                                                                              The present sequence is the S. pyogenes speB gene encoded extracellular protease. An immunoganic peptide derived from the proteese can be used in the proof. of antibody (Ab) and vaccine. Ab is prepid. By introducing the peptide into a mammal, pref. a Mouse, followed by Ab isolation. The Ab or a probe derived from the gene can be used for the diagnosis and detection of gp. A Streptococcus infections, while vaccine, which inhibits streptococcal replication, can be used to prevent and treat gp. A Streptococcus infections, and partic, to ameliorrate pharymitis, to saillitis, post-streptococcal glorentionephitis, sepisis, mannigitis, post-streptococcal glorentionephitis, sepisis, mannigitis, post-streptococcal glorentionephitis, sepisis, mannigitis, cellulitis, fascilitis and toxic shock like syndrome.
                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             detection, diagnosis |
pathogenic organisms,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1996-179944/18.
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                                                                                                                                                                                                                                                                                                 Local Similarity
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                         HVNWGWGGVSDGFFRLDALNPSALGTGGGAGGFNGYQSAVVG
                                                                ENFGYNOSVHQINRSDFS-QDWEAQIDKELSQNQPVYYQG-GKVGGHAFVIDGADGRNFY
                                                                                                                            AISTRQYNWNNILPTYSGRESNVQKMAISELMADVGISVDMDYGPSSGSAGSSRVQRALK 368
                                                                                                                                                                                 EKVKPGEQSFVGQHAATGCVATATAQIMKYHNYPNKGLKDYTYTLSSNNPYFNHPKNLFA
                                                                                                                                                                                                                        FMES-YVEQIKENKKLDT----TYAGTAEIKQPVVKSLLDSKGIHYNQGNPYNLLTPVI
                                                                                                                                                                                                                                        FTQSKYLMIYKDNETLDSNTQIEVYLTT---KQPVVKSLLDSKGIHYNQGNPYNLLTPVI 24B
                                                     ENFGYNQSVHQINRSDFSKQDWEAQIDKELSQNQPVYYQGVGKVGGHAFVIDGADGRNFY
                                                                                                            AISTROYNWNNILPTYSGRESNVQKMAISELMADVGISVDMDYGPSSGSAGSSRVQRALK
                                                                                                                                                                   EKVKPGEQSFVGQHAATGCVATATAQIMKYHNYPNKGLKDYTYTLSSNNPYFNHPKNLFA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Musser JA;
                                                                                                                                                                                                                                                                                                                                        398 AA;
                                                                                                                                                                                                                                                                                 Conservative
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382..398
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216
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333..338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note- "corresponding codon
                                                                                                                                                                                                                                                                                             53.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protease(s), partic. cysteine protease prevention and treatment of infection in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 97pp; English
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398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           partic. gp. A streptococcus strains
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                                                                                                                                                                                                                                                                               Score 1327.5;
Pred. No. 1.5e
5; Mismatches
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Co from a Steptococcus which expresses an extracellular protesse of a comprising a first member of a sample with an assay medalular comprising a first member of a specific binding has say medalular comprising a first member. On a specific binding has say medalular second member of the binding particles of the say where the first member has at least 1 epitopic site computer. Where the first epitopic site composition of the binding has a precision of the complex. Where the first epitopic site of the processe of the pathogen organism. The method is precisionally to the processe of the pathogen organism. The method is useful for screen presence of the pathogen organism. The method is streptococcus programs and semilarity epidence of infection with the streptococcus method diseases as waccine for proceeding softhe host. The process products are used monitoring the diseases streptococcus method diseases as waccine for proceeding softhe services of the process of the pathogen of infection with the lost. The process of th
                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 258; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Determining the presence of a Group A Streptococcus expressing a protense capable of degrading proteins of the extracellular matrix, using a specific antibody -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cysteine processe; spes; Group A Streptococcus; extracellunt, stin infection; detection; disapposis; extracellunar matrix; infection; stin infection; disease status monitoring; vaccine; Streptococcus mediated disease; pharyngitis; tonsillitis; scarlet fever; pestis; expsipalas; fascilitis; pneumonia; ecute rheumatic fever; poststreptococcul glomerulonephritis;
                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Column 7-8; 56pp;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; AAA07111.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cellulitis; bacteraemia; meningitis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  S. pyogenes cysteine protease speB7 protein sequence
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                                                                                                                                        FMES-YVEQIKENKKLDT-----TYAGTAEIKQPVVKSLLDSKGIHYNQGNPYNLLTPVI 173
                                                                                                                                                                  FTQSKYLMIYKDNETLDSNTQIEVYLTT---KQPVVKSLLDSKGIHYNQGNPYNLLTPVI 248
AISTRQYNWNNILPTYSGRESNVQKMAISELMADVGISVDMDYGPSSGSAGSSRVQRALK 368
                                                                     EKVKPGEQSFVGQHAATGCVATATAQIMKYHNYPNKGLKDYTYTLSSNNPYFNHPKNLFA
                                              EKYKPGEQSFYGQHAATGCYATATAQIMXYHNYPNKGLKDYTYTLSSNNPYFNHPKNLFA
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940S-0306542.
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                                                                                                                                                                                                                                                                53.1%;
                                                                                                                                                                                                                                                                Score 1327.5; DB
Pred. No. 1.5e-99;
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RESULT 4
ABP29579
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                                                         cs streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GAS (Streptococcus youngersaing one of $483 sequences [3]), given in the specification. The proteins have antibacterial and sequences can extinct [1], nucleic acids encoding [1], ARNG614-ARN7185 and proteins that bind [1] are used in the manufacture of medicaments for the treatment or prevention of infection or disease caused by streptococcus bacteria, particularly S. apalactiae and S. pyrogenes.

This is a streptococcus becteria, particularly S. apalactiae and S. pyrogenes. The streptococcus in a compound binds to prove the streptococcus in a compound binds to composition comprising [1] are used to detect Streptococcus in a compound binds to composition or disparation of the disease compound by may be used as a vaccius or the tis prevented or treated may be meningitian successive control of the streptococcus that is prevented or treated may be meningitian successive control of the streptococcus of the successive of
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Tettelin H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27-OCT-2000;
24-NOV-2000;
07-MAR-2001;
                                            Streptococcus proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to a protein (ABP25413-ABP30895) from group B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; Page 3948; 4525pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New Streptococcus protein for the treatment or prevention of infection or disease caused by Streptococcus bacteria, such as meningitis, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; ABN70210
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Streptococcus; GAS; GBS; group B streptococcus; Streptococcus agalactiae; group A streptococcus; Streptococcus pyogenes; antibacterial; antiinflammatory; infection; vaccine; meningitis; gene therapy.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            for detecting a compound that binds to the protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; 2000GB-0026333.
; 2000GB-0028727.
; 2001GB-0005640.
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Best Local S
Matches 257
The present sequence is given in a specification relating to novel oral bacterial polypeptide referred to as periodontain. The polypeptide has anidolytic activity for cleavage of denatured polypeptides non-denatured scripin polypeptides. It has anidolytic activity for cleavage of a non-denatured human alpha_1-proteinase inhibitor at a reactive site loop region of the inhibitor. Periodontain is useful for inhibiting the peptidase activity and reducting periodontitis, loss of tooth attachment and periodontal pocket formation, and for reducing
                                                                                                                           Novel oral bacterial periodontain polypeptide for diseases, has amidolytic activity for cleavage of alphal-proteinase inhibitor at reactive site loop
                                                                                                                                                                      WPI;
                                                                                                                                                                                                                                  (UYGE-)
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                                                                                              Example
                                                                                                                                                                                          Travis J,
                                                                                                                                                                                                              (POTE/)
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antibacterial;
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                                                                                                                                                                                                              POTEMPA J.
NELSON D.
                                                                                                                                                                                                                                UNIV GEORGIA
TRAVIS J.
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amidolytic; alpha_1-proteinase inhibitor; periodontit
                                                                                                                                                                                                                                                                                                                                                pyogenes
                                                                                                                                                                                                                                                                                                                                                                                                           pyogenes
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                                                                                                                                                                                                                                                                 9908-0130436
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                               entry)
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                                                                                                                                                                                                                                                                                                                                                                                                            streptopain.
                                                                                                                                                                                          Nelson
                                                                                              English.
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Pred. No. 3.2e
5; Mismatches
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                                                                                                                           treating periodontal non-denatured human region of inhibitor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            468
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                                                                                                                                                                                                                                                                                                                                                                             periodontitis;
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RESULT 6
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AC ANYTO A
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Best Local S
Matches 237
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ENGGYNGSVHQIMKSDXXKQDWEAQIDKELSQNQPYYYGG-GKVGGHAFVIGGAXGRNFY
ENGGYNGSXXXINKSDXXKQDWEAQIDKELSQNQPYYYGG-GKVGGHAFVIGGAXGRNFY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AISTROYNWNNILPTYSGRESNVOKMAISELMADVGISVDMDYGPSSGSAGSSRVORALK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HVNWGWGGVSDGFEHLDALNPSALGTGGGAGGFNGYQSAVXG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HVNWGWGGVSDGFFRLDALNPSALGTGGGAGGFNGYQSAVVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          XISTRQYNWNNILPTYSGRESNVQKMAKSELMADVGISVDMDXXPSSGSAGSSRVQRALX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EKYKPGEQSFYGQHAATGCYATATAQIMKYHNXPNKGLKXYTYTLSSNNPYFNHPKNLXX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EXVKPGEQSFVGQHAATGCVATATAQIMKYHNYPNKGLKDYTYTLSSNNPYFNHPKNLFA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FTQSKYLMIYKDNETLDSNTQIEVYLTT---KQPVVKSLLDSKGIHYNQGNPYNLLTPVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        398 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .2e-89
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Superantigen toxin; SAg; Streptococcal pyrogenic exotoxin A; SBE-A; antheoterial; vaccine; MHC class II receptor; T-cell antigen receptor; cytostatic; antibody; staphylococcal/streptococcal toxin; toxid; SPEA4 diagnosis; treatment; superantigen-associated bacterial infection.
                                                                                                                              Streptococcus
                                                                                                                                                                                                                                                                                    Streptococcal
                                                                                                                                                                                                                                                                                                                              05-JUN-2000
                                                                                                                                                                                                                                                                                                                                                                        AAY70109;
                                             24-FEB-2000
                                                                                       WO200009154-A1
                                                                                                                                                                                                                                                                                                                                                                                                               AAY70109
13-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                                                               standard;
                                                                                                                                                                                                                                                                                                                           (first
                                                                                                                              sp.
                                                                                                                                                                                                                                                                                 pyrogenic exotoxin A (SPE-A).
98WO-US16766
                                                                                                                                                                                                                                                                                                                                                                                                               Protein;
                                                                                                                                                                                                                                                                                                                           entry)
                                                                                                                                                                                                                                                                                                                                                                                                               251
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SPEA42;

The present amino acid sequence is the Streptococcal pyrog exotoxin A (SPE-A), a bacterial superantigen toxin (SAg), formulation of SPE-A vaccine SPEAA2. The coding region of is altered by site directed mutagenesis, introducing L42R

Nucleic acid diagnosis of

encoding superantigen toxin useful as a vacc superantigen-associated bacterial infections

vaccine

and

for

pyrogenic this

SAg

the toxin that

Page 94-95;

118pp;

English

WPI; 2000-224177/19. N-PSDB; AAZ51112.

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Olson MA,

Bavari

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(REED-) REED ARMY INST RES WALTER.

13-AUG-1998;

98WO-US16766

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RESULT 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      results in disruption of binding of the toxin to both the MHC class II or T-cell antigen receptor. SPF-A has antibacterial and cytostatic activity This sequence is useful for the production of SPE-A vaccines and specific antibodies. This vaccine overcomes the disadvantages of the chemically inactivated toxoids and is designed to protect individuals against one or several related stabbylococcal and streptococcal toxins. It is used for the disgnosis and treatment or amelioration of superantigen-associated bacterial infections.
The present sequence is the protein sequence of Streptococcus pyogenes vaccine SPEA4. The vaccine differs from the native sequence by substitution of the Leu-42 residue by Arg. This mutation is expected to disrupt contact between the toxin and
                                                                                                                                                                                                         01-SEP-1998;
                                                                                                                                                                                                                              04-JUN-2002
                                                                                                                                                                                                                                                  US6399332-B
                                                                                                                                                                                                                                                                                                   attenuation; mutant; mutein.
                                                                                                                                                                                                                                                                                                                              Streptococcal pyrogenic exotoxin A vaccine SPEa42
                                                                                                                                                                                                                                                                                                                                                     23-SEP-2002
                                                                                                                                                                                                                                                                                                                                                                       ABB79508
                                                                                                                                                                                                                                                                                                                                                                                           ABB79508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                     Novel isolated and purified superantigen toxin DNA fragment which has
been genetically altered, useful for producing vaccine for treatment of
superantigen toxin-associated bacterial diseases
                                                                                                                                                               (USSA ) US SEC
                                                                                                                                                                                     25-JUN-1997;
                                                                                                                                                                                                                                                                     Synthetic.
                                                                                                                                                                                                                                                                               Streptococcus
                                                                                                                                                                                                                                                                                                             Exotoxin A;
                                                   Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
les 217; Conserv
                                                                                                               2002-546281/58.
DB; ABN84229.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     151
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                                                                                                                                             RG,
                                                                                                                                                                                                                                                                                                                                                                                           standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ELKNQEMATLFKDKNIDIYGVEYYHLCYLCENAERSACI-GGVTNREGNHLEIPKKIVVK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QQDPDPSQLHRSSLVKNLQNIYFLYEGDPVTHENVKSVDQLRSHDLIYNVSGPNYDKLKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VSIDGIQSLSFDIETNKKWYTAQELDYKVRKYLTDNKQLYTNGPSKYETGYIKFIPKNKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VSIDGIQSLSFDIETNKKMYTAQELDYKVRKYLTDNKQLYTNGPSKYETGYIKFIPKNKE 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QQDPDPSQLHRSSLVKNLQNIYFLYEGDPVTHENVKSVDQLRSHDLIYNVSGPNYDKLKT
                                                                                                                                                                                                                                                                                                                                                                                                                                             SFWFDFFPEPEFTQSKYLMIYKDNETLDSNTSQIEVYLTTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                       SFWFDFFPEPEFTQSKYLMIYKDNETLDSNT-QIEVYLTTK 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ELKNQEMATLFKDKNVDIYGVEYYHLCYLCENAERSACIYGGVTNHEGNHLEIPKKIVVK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     251 AA;
                                                                                                                                                                                                                                                                                                             SPEa; SPEa42; superantigen; antigen; toxin; vaccine;
                                                   Column
                                                                                                                                             Olson MA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                             pyogenes.
                                                                                                                                                                 OF ARMY
                                                                                                                                                                                     97US-0882431.
                                                                                                                                                                                                         98US-0144776.
                                                                                                                                                                                                                                                                                                                                                                                           Protein;
                                                 63-65; 46pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98.28;
                                                                                                                                             Bavari
                                                                                                                                                                                                                                                                                                                                                                                           251
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                   English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 21;
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                      SPEa
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the

Tumor cell capable of stimulating antitumor immune reactivity in vitro or in vivo comprises exogenous nucleic acids encoding a superantigen and a costimulatory molecule

WPI;

2001-158657/16

DS

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RESULT 8
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Best Local
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                                    31-JAN-1994;
19-JUN-1995;
03-OCT-1999;
17-JAN-1990;
17-JAN-1991;
01-JUN-1992;
02-MAR-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HIA-DR receptor, reducing DRI binding. SPEA/2 can be expressed as a recombinant protein in Escherichia coll as a secreted protein or as a cytoplasmic product. No indicators of toxicity have been detected for the purified recombinant protein, and vaccine studies demonstrate that SPEA/2 is highly antigenic, inducing protective immunity in a mouse animal model. The attenuated superantigen can be used to protect against superantigen toxin infections. Methods producing and using altered superantigen toxins as vaccines, and in diagnosis and therapy, are provided by the invention. A multival in vaccine consisting of altered superantigen toxins from SRA, SEB, SEC-1, TSST-1 and SPEA is predicted to provide protective immunity against the majority of bacterial superantigen toxins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                             30-JAN-2001.
                                                                                                                                                                                                                                                                                        US6180097-B1
                                                                                                                                                                                                                                                                                                                            Streptococcus
                                                                                                                                                                                                                                                                                                                                                                    Tumour;
                                                                                                                                                                                                                                                                                                                                                                                                            Streptococcus pyrogenes toxin A protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB67344;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAB67344 standard; peptide;
(TERM/) TERMAN
                                                                                                                                                                                                        30-OCT-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                      23-APR-2001
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                                                                                                                                                                                                                                                                                                                                                                       cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ELKNOEMATLFKOKNUDIYGVEYYHLCYLCENAERSACI-GOVUNRGONHLEIDKKIVYK
ELKNOEMATLFKOKNUDIYGVEYYHLCYLCENAERSACITGGVUNHEONHLEIDKKIVYK
ELKNOEMATLFKDKNVDIYGVEYYHLCYLCENAERSACITGGVUNHEONHLEIDKKIVVK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SFWEDEFEREPETTOSKYLMIYKDNETLDSNT-QIEVYLTTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VSIDGIQSLSFDIETNKKMYTAQELDYKVRKYLTDNKQLYTNGPSKYETGYIKFIPKNKE 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VSIDGIQSLSFDIETNKKMYTAQELDYKVRKYLTDNKQLYTNGPSKYETGYIKFIPKNKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 251 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                            pyogenes
                                                                                                                   94US-0189424.
95US-0491746.
89US-0416530.
  D
S
                                          93US
                                                           91WO-US00342
92US-0891718
                                                                                                                                                                                                        98US-0183437
                                                                                                     90US-0466577
                                                                                                                                                                                                                                                                                                                                                                    immune;
                                          -0025144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   45.4%;
                                                                                                                                                                                                                                                                                                                                                                       enterotoxin
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    Mismatches

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Pred. No. 3e-84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ₹
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23;
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AAR13209
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local S
Matches 216
SPE A can be used for tumouricidal treatment, esp. with a haemolysin. Synthetic polypeptides having structural homology to Streptococcal pyrogenic exotoxins are claimed, provided the homology includes statistically significant sequence homology, alignment of Cysteine
                                                                  Disclosure;
                                                                                     Treating cancer with enterotoxin from Staphylococcus aureus -
administered by IV injection, having same tumoricidal activity
as Staphylococcal protein A without potential toxic reactions
                                                                                                                                                                                                                  17-JAN-1990;
                                                                                                                                                                                                                                                                                                                  Streptococcus
                                                                                                                                                                                                                                                                                                                                            SPE A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention relates to a tumour cell capable of atimulating antitumor immune reactivity in vitro or in vivo contains and expresses an exogenous nucleic acid molecule encoding a superantigen or its active fragment and an exogenous nucleic acid molecule encoding a costimulatory molecule that activates T cells in conjunction with an antigenic stimulus. The invention may be used
                                                                                                                                           WPI; 1991-237984/32.
                                                                                                                                                                     Terman
                                                                                                                                                                                           (TERM/) TERMAN D
                                                                                                                                                                                                                                          17-JAN-1991;
                                                                                                                                                                                                                                                                   25-JUL-1991
                                                                                                                                                                                                                                                                                           W09110680-A
                                                                                                                                                                                                                                                                                                                                                                    Streptococcal
                                                                                                                                                                                                                                                                                                                                                                                              15-OCT-1991
                                                                                                                                                                                                                                                                                                                                                                                                                       AAR13209
                                                                                                                                                                                                                                                                                                                                                                                                                                            AAR13209 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure;
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216; Conger
                                                                                                                                                                                                                                                                                                                                            cancer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cer therapy by stimulating an anticancer immune response or ex vivo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VSIDGIQSLSFDIETNKKMVTAQELDYKVRKYLTDNKQLYTNGPSKYETGYIKFIPKNKE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ELKNQEMATLFKDKNVDIYGVEYYHLCYLCENAERSACIYGGVTNHEGNHLEIPKKIVVK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ELKNQEMATLFKDKNIDIYGVEYYHLCYLCENAERSACI-GGYTNREGNHLEIPKKIVVK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VSIDGIQSLSFDIETNKKMVTAQELDYKVRKYLTDNKQLYTNGPSKYETGYIKFIPKNKE
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                                                                Fig
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                                                                                                                                                                                                                                                                                                                    NY-5
                                                                                                                                                                                                                                                                                                                                                                   pyrogenic enterotoxin
                                                                                                                                                                                                                                                                                                                                          treatment; pyrogen;
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                                                                                                                                                                                                                                          91WO-US00342
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                                                              74pp;
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                                                                                                                                                                                                                                                                                                                    strain
                                                                                                                                                                                                                                                                                                                                                                                                                                             Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    45.2%;
                                                                English.
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Pred. No. 9.2e-84;
1; Mismatches 2
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                                                                                                                                                                                                                                                                                                                                          tumouricide;
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                                                                                                                                                                                                                                                                                                                                          scarlet fever
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RESULT 10
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                                                                                                                                                                                                                                 Staphylococcus
                                                                                                                                                                                                                                                        Staphylococcal
                                                                                                                                                                                                                                                                     Staphylococcal
                                                                                                                                                                                                                                                                                     08-JUN-1994
                                                                                                                                                                                                                                                                                                   AAR45017;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    residues and similar hydropathy profiles See AAR13203-R13211.
                                                                                                                                                                                                                                                aucormmune
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                                                                                                                                                                                                                                                                                                                 standard;
                                                                                                                                                                                                                                                                                                                                                      SFWFDLFPEPEFTQSKYLMIYKDNETLDSNTSQIEVYLTTK
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                                                                                                                                                                                                                                                disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      221 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                       enterotoxin;
                                                                                                                                                                                                                                                                     enterotoxin
                                                                                                                                                                                                                                                                                                                 protein;
                                                                                                                                                                                                                                               toxicity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               97.38;
                                                                                                                                                                                                                                                                     SPE
                                                                                                                                                                                                                                                        SE;
                                                                                                                                                                                                                                                                                                                  221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 1123; DB 12
Pred. No. 2.8e-83;
1; Mismatches 3
                                                                                                                                                                                                                                                Protein
                                                                                                                                                                                                                                                      cancer; tumouricidal agent;
                                                                                                                                                                                                                                               ?
                                                                                                                                                                                                                                               perfusion system.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length
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01-JUN-1993;
                      09-DEC-1993
                                          V09324136-A
                                                               aureus
93WO-US05213
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Use of staphylococcal enterotoxin(s) and homologues - for treating cancer in a patient or for the treatment of auto-immune Stone JL, (STON/) STONE J L. diseases WPI; 1993-405418/50. 01-JUN-1992; Terman 9205-0891718 DS

Disclosure; Fig 1; 90pp; English

tumouricidal agents for treating cancers and aucoimmune disease thmouricidal activity and toxicity identical to that they exhibit tumouricidal activity and toxicity identical to that observed for the Protein A perfusion system. They may be administ The sequences given in ARR4501:-21 are Staphylococcal enterotoxins which may be used in the methods of the invention for treating can in a patient. These SEs, and homologues of them, can be used as 1.V. injection. administered cancer (SES)

Sequence 221 AA;

Query Match

44.98;

Score 1123;

DB

14;

Length 221;

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N

Matches

Conservative

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Pred. No. 2.8 1; Mismatches

. 2.8e-83;

Indels

2; Gaps

61 Ņ

97.3%;

Best Local Similarity

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19-JUN-1995;
03-OCT-1989;
17-JAN-1990;
17-JAN-1991;
01-JUN-1992;
The present sequence is the protein sequence of exotoxin A (SPE A) of Streptococcus pyogenes. Similarity is shown, in several streptococcus pyogenes. Similarity is shown, in several streptococcal enterotoxins, streptococcal pyrogenic exotoxins and staphylococcal extoliative toxins (see ABB7623-44). In the present invention, synthetic polypeptides useful in tumour therapy and in blocking or destroying autoreactive r and B lymphocyte populations are characterised by substantial structural homology to staphylococcal enterotoxin A and enterotoxin B and to streptococcal pyrogenic exotoxins, with statistically significant sequence homology and similarity (value of Lipman and Pearson algorithm in Monte Carlo analysis exceeding to include alignment of cysteine residues and similar hydropathy
                                                                                                                                                             Reagent for treating cancer without the comprises a specific V beta subset of T tumor and stimulated with superantigens
                                                                                                                                                                                                                                                                                                                                                                                                                                               Exotoxin A; antitumour;
                                                                                                                                           Disclosure;
                                                                                                                                                                                                        WPI; 2002-415198/44
                                                                                                                                                                                                                                                  (TERM/) TERMAN
                                                                                                                                                                                                                                                                       02-MAR-1993;
                                                                                                                                                                                                                                                                                                                                                             19-DEC-2000;
                                                                                                                                                                                                                                                                                                                                                                                                     US2002051765-A1
                                                                                                                                                                                                                                                                                                                                                                                                                         Streptococcus pyogenes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Staphylococcus pyogenes exotoxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    09-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABB76240 standard;
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                                                                                                                                         Fig
                                                                                                                                                                                                                                                                                                                                                                                                                                               SPE A; superantigen; antigen; tumour; cancer;
therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                           2000US-0741503
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91WO-US00342.
92US-0891718.
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95US-0491746.
89US-0416530.
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                                                                                                                                                                                                                                                                       93US-0025144
                                                                                                                                         2
                                                                                                                                        17.pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Protein;
                                                                                                                                                                       cancer without the need for e.g. radiotherapy, V beta subset of T cells sensitized to a growing
                                                                                                                                         English.
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Mutant SPE-A toxin with at least substantially non-lethal - used
                                                                                                                                                                                                                                                                                                                                                                      04-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                           AAW12097;
                                                                                                                                                                                                                                                                                                                                                                                                                AAW12097
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tumouricidal reaction.
                                                                                                          07-JUN-1995;
                                                                                                                             07-JUN-1996;
                                                                                                                                                                         W09640930-A1
                                                                                                                                                                                                       Peptide
                                                                                                                                                                                                                                                           Streptococcus
                                                                                   (MINU ) UNIV
                                                                                                                                                    19-DEC-1996
                                                                                                                                                                                                                            Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local
                                1997-099936/09
DB; AAW12097.
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                                                                                                                                                                                                                                                                                                                                                                                                              standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    221 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                     MINNESOTA
                                                                                                                                                                                                                                                           pyogenes
                                                                                                                                                                                                                                                                                                                                               pyogenes Streptococcal toxin
                                                              Roggiani
                                                                                                                               96WO-US10252
                                                                                                                                                                                                       /label= sig_peptide
31..251
                                                                                                                                                                                            /label- mat_peptide
                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   97.38;
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                                                                 Schlievert
                                                                                                                                                                                                                                                                                                                                                                                                                251
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Pred. No. 2.8e-83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
 one amino acid change is
in vaccine composition for
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profiles. These superantigens are used to treat solid tumours, including their metastases, without rediation, surgery or standard chemotherapeutic agents. A claimed method of human cancer treatment involves contacting haematopoietic cells from a patient with one or more superantigens ex vivo to generate stimulated cells, selecting a specific v beta subset of cells, and reintroducing hese cells into the patient to induce an in vivo therapeutic,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   vaccine; protection; treatment; cancer; neutralising antibody; streptococcal toxic shock syndrome; STSS; symptom; amelioration; fever; hypotension; group A streptococcal infection; myositis; fascitis; liver damage; T cell; lymphoma; ovarian; uterine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Streptococcal; toxin A; SPE-A; non-lethal; mutant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOTAL THE CONTROL OF 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     or The present sequence is Streptococcus progenes Streptococcus to tain A (SBF-A), from which a non-lethal mutant SBF-A, comprising at least 1 amino acid change, can be derived. The mutant SBF-A can be used to produce vencious to an object and sequence streptococcus to the sequence of 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local
Matches 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                        N-PSDB;
                                     WPI; 1998-333330/29
                                                                    Ohlendorf D,
                                                                                                                                   06-DEC-1996;
                                                                                                                                                                  05-DEC-1997;
                                                                                                                                                                                                 11-JUN-1998
                                                                                                                                                                                                                                                                                                    SPP-A toxin; nonlethal; mutant; Streptococcus pyogenes exotoxin a; wild type; nontoxic; antibody; vaccine; immunity; ovarian cancer; streptococcal toxic shock syndrome; STSS; T cell lymphoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW59780 standard; Protein;
                                                                                                  (MINU ) UNIV
                                                                                                                                                                                                                                W09824911-A2
                                                                                                                                                                                                                                                            Streptococcus
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                                                                                                                                                                                                                                                                                                                                                                    Amino acid sequence of Streptococcus pyogenes exotoxin
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215; Conserv
                        AAV41593
                                                                                                                                                                                                                                                                                             cancer.
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                                                                                                     MINNESOTA
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                                                                    Roggiani
                                                                                                                                 96US-0032930
                                                                                                                                                                  97WO-US22228
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                                                                    Schlievert
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Pred. No. 4.1e-83;
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    RESULT 14
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Best Local Similarity
Matches 215; Conserv
07-JUN-1996;
                                   19-DEC-1996
                                                                                                             Misc-difference
                                                                                                                                                                                                                         Streptococcus
Synthetic.
                                                                                                                                                                                                                                                                                                                                                                    Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                   04-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW12154;
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                                                               709640930-A
                                                                                                                                                                           Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
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96WO-US10252
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This is the amino acid sequence of the Streptococcus pyogenes exotoxin A (SPEPA toxin). The novel mutant Streptococcal SPEPA toxin has at least 1 as change and is nonlethal compared with a protein to wild type SPEPA toxin. The mutant SPEPA toxins are nontoxic and can produce antibodies that neutralise wild type SPEPA toxin activity. The toxins can be used in vaccines and therapeutics to generate a protective immune response against streptococcal infection. They can be used to protect against the development of streptococcal infection. They can be used for the streptococcal infection or STSS and in methods for stimulating real proliferation and in the treatment of ceneer. In particular they can be used for treating rainals with symptoms of
211 SFWFDFFPEPEFTQSKYLMIYKDNETLDSNTSQIEVYLTTK
                                                                                                                                                                VSIDGIQSLSFDIETNKKMVTAQELDYKVRKYLTDNKQLYTNGPSKYETGYIKFIPKNKE 180
                                                                                                                                                                                                                                                                                                                                                                                                                 QQDPDPSQLHRSSLVKNLQNIYFLYEGDPVTHENVKSVDQLRSHDLIYNVSGPNYDKLKT
                                                              SEWEDEFPERETOSKYLMIYKDNETLDSNT-QIEVYLTTK 220
                                                                                                                        VSIDGIQSLSFDIETNKKMYTAQELDYKVRKYLTDNKQLYTNGPSKYETGYIKFIPKNKE
                                                                                                                                                                                                                                                     ELKNQEMATLFKDKNVDIYGVEYYHLCYLCENAERSACIYGGVTNHEGNHLEIPKKIVVK
                                                                                                                                                                                                                                                                                                               ELKNOEMATLFKDKNIDIYGVEYYHLCYLCENAERSACI-GGVTNREGNHLEIPKKIVVK 120
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Pred. No. 4.1e-83;
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vaccine; protection; treatment; cancer; neutralising antibody; streptococcal toxic shock syndrome; STSS; symptom; amelitoration; fever; hypotension; group A streptococcal infection; myositis; fascitis; liver damage; T cell; lymphoma; ovarian; uterine.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW12154 standard; Protein;
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                                                                                                                                                                                                                                            pyogenes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               pyogenes Streptococcal toxin A mutant Ser195Ala.
                              /label- mat_peptide
225
/note= "wild type Ser
                                                                                                         /label- sig_peptide
                                                                                                                                                                 Location/Qualifiers
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   replaced
   ьy
   Ala.
                                                                                                                                                                                                                                                                                                                                                                                                          production;
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RESULT 15
ANH12146
ANH12146
XX ANH12
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XX Strep
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Sequence not given in the specification, but constructed toxic toxic playen in the specification, but constructed toxic standard process of the wild type SPEA sequence given on pages 77-79.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                           Streptococcal; toxin A, SBE-A; non-lethal; mutant; production; vacche; protection; treatment; cancer; neutralising antibody; streptococcal toxic shock syndrome; STSS; symptom; amelioration; fever; hypotension; group A streptococcal infection; myositis; fascitis; liver damage; T cell; lymphoma; ovarian; uterine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mutant SPE-A toxin with at least one amino acid change is
substantially non-lethal - used in vaccine composition for
treatment of cancer and streptococcal toxic shock syndrome etc.
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                                      Streptococcus
Synthetic.
                                                                                                                                                                                                                  Streptococcus pyogenes Streptococcal toxin A mutant Lys157Glu.
                                                                                                                                                                                                                                                              04-NOV-1997
                                                                                                                                                                                                                                                                                                                                       AAW12146 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 07-JUN-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1997-099936/09
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62 ELKNQEWATLFKDKNIDIYGVEYYHLCYLCENAERSACI-GGYTNREGNHLEIPKKIVVK
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nilarity 96.8%;
Conservative
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                                                          pyogenes
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  Location/Qualifiers
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20 MB. Sequence not given in the specification, but constructed cusing the wild type SPEA sequence given on pages 77-79.
                                                                                                                                                                                                                                           Query Match
Best Local S
Matches 214
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substantially non-lethal - used in vaccine composition for
treatment of cancer and streptococcal toxic shock syndrome etc.
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                                                                                                                 SFWFDFFPEPEFTQSKYLMIYKDNETLDSNT-QIEVYLTTK
                                                                                                                                                                              QQDPDPSQLHRSSLVKNLQNIYFLYEGDPVTHENVKSVDQLLSHHLIYNVSGPNYDKLKT
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                                                            VSIDGIQSLSFDIETNKKMVTAQELDYKVRKYLTDNEQLYTNGPSKYETGYIKFIPKNKE
SEWEDEEPEETQSKYLMIYKDNETLDSNTSQIEVYLTTK
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187
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                                                                                                                                                                                                                                                       44.7%;
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                                                                                                                                                                                                                                         Score 1118; DB 18;
Pred. No. 8.7e-83;
2; Mismatches 3;
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Result
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Maximum Match 100%
Listing first 45 summaries
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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/ cgin2_6/ptcdata/1/pubpas/ISS6_NEW_PIB Pigp: *
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Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-870-759-20

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US-10-002-784A-10

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                              Sequence 16.
Sequence 13.
Sequence 23.
Sequence 27.
Sequence 20.
Sequence 10.
Sequence 11.
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Sequence 12.
Sequence 12.
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26, App.
27, App.
28, App.
29, App.
20, App.
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20 340 25.7 258 9 US-09-870-759-14 Sequence 14, Appl. 22 307 23.2 227 9 US-10-027-84A-2 Sequence 24, Appl. 23 307 23.2 227 9 US-10-027-84A-2 Sequence 2, Appl. 23 31.5 22.0 23.3 9 US-10-027-84A-4 Sequence 2, Appl. 25 21.5 22.0 23.3 9 US-090-766-4 Sequence 4, Appl. 26 21.5 22.0 23.3 9 US-090-766-7 Sequence 4, Appl. 27 28 28 29 29 US-10-283-838-7 Sequence 6, Appl. 28 29.5 21.9 23.3 9 US-090-766-7 Sequence 6, Appl. 28 29.5 21.9 23.3 9 US-090-766-5 Sequence 6, Appl. 28 29.5 21.9 23.3 9 US-090-766-3 Sequence 6, Appl. 28 29.5 21.9 23.3 9 US-090-766-3 Sequence 6, Appl. 28 29.5 21.4 23.3 1 US-08-870-759-16 Sequence 6, Appl. 28 29.5 21.9 23.3 9 US-090-766-3 Sequence 6, Appl. 28 29.5 21.0 23.3 9 US-090-766-3 Sequence 6, Appl. 28 29.5 21.0 23.3 9 US-090-766-3 Sequence 6, Appl. 28 29.5 21.0 23.3 9 US-090-766-3 Sequence 6, Appl. 28 29.5 21.0 23.3 9 US-090-766-1 Sequence 7, Appl. 28 29.5 21.0 23.3 9 US-090-766-1 Sequence 7, Appl. 26 25 25 29.5 US-090-766-1 Sequence 1, Appl. 27 28 29.5 US-090-766-1 Sequence 3, Appl. 27 29 US-090-766-1 Sequence 3, Appl. 28 29.5 21.8 89 US-10-002-784A-3 Sequence 3, Appl. 28 29.5 21.8 89 US-10-002-784A-3 Sequence 3, Appl. 29 US-10-002-784A-3 Sequence 1, Appl. 20 US-10-002-784A																										
25.7 25.8 9 US-09-870-759-14 Sequence 14, 23, 25, 25, 7 US-08-887-471-2 Sequence 24, 23, 25, 25, 7 US-08-887-471-2 Sequence 24, 25, 25, 25, 25, 25, 25, 25, 25, 25, 25	45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20
5257 9 US-09-870-759-14 Sequence 14, 5257 1 US-08-882-431-2 Sequence 2, 2557 9 US-10-820-784A-4 Sequence 2, 2557 9 US-10-002-784A-4 Sequence 2, 2557 9 US-10-002-784A-4 Sequence 4, 2557 9 US-09-900-766-4 Sequence 6, 2559 9 US-09-900-766-7 Sequence 6, 2559 9 US-09-900-766-7 Sequence 7, 2559 9 US-09-900-766-5 Sequence 8, 2559 9 US-09-900-766-3 Sequence 16, 2559 9 US-09-900-766-3 Sequence 2, 2559 9 US-09-900-766-3 Sequence 3, 2559 9 US-09-900-766-3 Sequence 6, 2559 9 US-09-9000-766-3 Sequence 6, 2559 9 US-09-9000-766-3 Sequence 6, 2559 9 U	109	115	116	117.5	120	151	182.5	209.5	213.5	213.5	263.5	263.5	277.5	281.5	283.5	289	289.5	289.5	290.5	291.5	291.5	291.5	307	307	311	340
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Sequence 1.4 Sequence 2.5 Sequence 3.5 Sequence 4.5 Sequence 4.5 Sequence 6.5 Sequence 7.5 Sequence 1.6 Sequence 1.6 Sequence 1.6 Sequence 2.7 Sequence 3.7 Seque	φ	9	9	_	9	9	9	9	9	9	9	9	ø	9	_	9	9	9	φ	φ	9	φ	9	_	9	9
133335687	US-09-870-759-18	US-10-002-784A-32	US-10-002-784A-12	US-08-882-431-12	US-10-002-784A-34	US-10-002-784A-33	US-10-002-784A-35	US-10-002-784A-36	US-10-002-784A-38	US-10-002-784A-37	US-09-900-766-1	US-09-900-766-2	US-09-900-766-3	US-09-900-766-5	US-08-882-431-4	US-09-870-759-16	US-10-283-838-8	us-09-900-766-7	US-09-900-766-6	US-10-283-838-7	US-09-900-766-4	US-10-002-784A-4	US-10-002-784A-2	US-08-882-431-2	US-09-870-759-8	US-09-870-759-14
														Sequence 5	Sequence 4.	Sequence 10					Sequence 4	Sequence 4,				Sequence 1
Appl Appl Appl Appl Appl Appl Appl Appl	•	•	•	•	•	-	-	•	•	-	•	•	•	`	`	٠,	•	•	`	`	`	` A	`	`	` >	
	Appl	App1	App1	App1	App1	Appl	Appl	App1	App1	Appl	ppli	ppli	ppli	pp11	pp11	App1	pp11	ppli	ppli	ppli	ppli	ppli	ppli	ppli	ppli	Appl

ALIGNMENTS

US-08-882-431-16 ; Sequence 16, Ap ; Publication No.

GENERAL INFORMATION:

Application US/08882431
No. US20030009015A1
ORMATION:
Robert G. Ulrich,
Mark A. Olson

APPLICANT: Robert G. U. APPLICANT: Mark A. Olso APPLICANT: Sina Bavari

TITLE OF INVENTION: Bacterial Superantigen
TITLE OF INVENTION: Vaccines

NUMBER OF SEQUENCES:

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TELEFAX: (301) 619-7714
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: Apple Mediatosh 7.:
OPERATING SYSTEM: Mediatosh 7.:
SOFTWARE: Microsoft Word 6.0
CURRENT APPLICATION DATA:
                                                                                                          NAME: HOTAN, JOHN
REGISTRATION NUMBER: 26,313
REFERENCE, POCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 619-2065
                                                                                                                                                                                             FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Moran, John
                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                 SEQUENCE CHARACTERISTICS:
LENGTH: 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: John Moran
STREET: US Army MRMC
CITY: FORT DETRICK
                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/
FILING DATE: June 25, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: MARYLAND
STRANDEDNESS:
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21702-5012
                Amino Acid
Unknown
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; MOLECULE TYPE: Peptide
US-08-882-431-16
                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local S
Matches 251
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PRIOR FILING DATE: 97-06-25; 98-09-01
NUMBER OF SEQ ID NOS: 40
SOFTMARE: Apple Macintosh Microsoft Word 6.0
SEQ ID NO 16
LENGTH: 211
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 16, Application US/10002784A Publication No. US20030036644A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
Matches 251; Conserva
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: Bacterial Superantigen Vaccines FILE REFERENCE: 003/233/SAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Ulrich, Robert G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Artificial sequence
        241 TSQIEVYLTTK 25:
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                                        ENAERSACIYGGYTNHEGNHLEIPKKIYVKVSIDGIQSLSFDIETNKKMYTAQELDYKVR
                                                                                                                                                                                                                 THENVKSVDQLRSHDLIYNVSGPNYDKLKTELKNQEMATLFKDKNVDIYGVEYYHLCYLC
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                                                                                                                   ENAERSACIYGGVTNHEGNHLEIPKKIVVKVSIDGIQSLSFDIETNKKMVTAQELDYKVR
                                                                                                                                                                                              THENVKSVDQLRSHDLIYNVSGPNYDKLKTELKNQEMATLFKDKNVDIYGVEYYHLCYLC
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                                                                                                                                                                                                                                                                                                                                                 Score 1322; DB 9;
Pred. No. 9.5e-110;
); Mismatches 0;
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Pred. No. 9.5e-110;
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                                APPLICANT: ULITCH, Robert G.
TITLE OF INTERTION BACKETAI Superantigen Vaccines
FILE REFERBEGE 00/233/SAP
CURRENT SPLICATION NUMBER: US/10/002,784A
CURRENT FILING DATE: 2001-11-26
PRIOR APPLICATION NUMBER: 00/982 431; 09/144,776
PRIOR PRILICANTON NUMBER: 07/982 431; 09/144,776
PRIOR PRILICANTON NUMBER: 07/982 431; 09/144,776
PRIOR SEGO ID NOS: 40
NUMBER: 07 SSQ ID NOS: 40
SOPTWARE: APPLE MACINTUSH MICROSOFT WORD 6.0
SOPTWARE: APPLE MACINTUSH MICROSOFT WORD 6.0
LENGTH: 20
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US-10-002-784A-26
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                                                                                                                                                                                                                                                                                    Sequence 26, Application US/10002784A Publication No. US20030036644A1
                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 13, Application US/08973391A Patent No. US20020054887A1 GENERAL INFORMATION:
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CUBRENT FLINE DATE: 198-03-12
PRIOR APPLICATION NUMBER: PCT/US96/10252
PRIOR FILING DATE: 1996-06-07
PRIOR APPLICATION NUMBER: US 06/480,261
PRIOR APPLICATION THE PRIOR FLINE DATE: 1995-06-07
NUMBER: OF SEG ID NOS: 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: ROGGIANI, MANUELA
APPLICANT: ROCOH, Jennifer
APPLICANT: Oblendorf, Douglas
TITLE DE INVENTION: MUTANTS OF STREPTOCOCCAL TOXIN A AND METHODS
FILE REFERENCE: 600.3110800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Schlievert, Patrick M. APPLICANT: Roggiani, Manuela
ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOCAL
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241 TSQIEVYLTTK 251
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 ENAERSACIYGGYTNHEGNHLEIPKKIYVKYSIDGIQSLSFDIETNKKMYTAQELDYKYR 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               181 KYLTDNKQLYTNGPSKYETGYIKFIPKNKESFWFDFFPEPEFTQSKYLMIYKDNETLDSN 240
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61 THENVKSYDOLLSHHLIKNYSGENYDKLÆTELKAGEMATLFKDKNODIYGVEYYHLCYLC 120
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99.2%; Pred. No. 1.7e-108;
tive 0; Mismatches 2;
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; OTHER INFORMATION: mutant streptococcal pyrogenic exotoxin-A
US-10-002-7844-26
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                                  RESULT 6
US-09-870-759-20
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CURRENT FILING DATE: 2001-11-26
PRIOR APPLICATION NUMBER: 05/882,431; 09/144,776
PRIOR FILING DATE: 97-06-25; 98-09-01
NUMBER OF SEQ ID NOS: 40
SOFTMARE: Apple Macintosh Microsoft Word 6.0
SEQ ID NO 27
SEQ ID NO 27
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Best Local
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sequence 20, Application US/09870759
Patent No. US20020177551A1
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TITLE OF INVENTION: Bacterial Superantigen Vaccines
FILE REFERENCE: 003/233/SAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
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mes 217; Conserv
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181 SFWFDFFPBPETTQSKYLMIYKDNETLDSNT-QIEVYLTTK 220
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                                                                                                        ELKNQEMATLFKDKNVDIYGVEYYHLCYLCENAERSACIYGGVTNHEGNHLEIPKKIVVK 150
                                                                                                                                                                              VSIDGIQSLSFDIETNKKMVTAQELDYKVRKYLTDNKQLYTNGPSKYETGYIKFIPKNKE 180
                                                                                                                                                                                                                                                                                                                       QQDPDPSQLHRSSLVKNLQNIYFLYEGDPVTHENVKSVDQLRSHDLIYNVSGPNYDKLKT
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98.2%;
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Pred. No. 7.3e:
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Pred. No. 2.7e-93;
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GENERAL INFORMATION:
APPLICANT TENNAS, DAVID S
TITLE OF INVENTION: COMPOSITIONS AND METHODS
FILE REFERENCE: 870759
CURRENT PRILICATION NUMBER: US/09/870,759
CURRENT FILING DATE: 2002-01-14
PRIOS APPLICATION NUMBER: US/06/208,128
PRIOR FILING DATE: 2000-05-30
NUMBER: 05 SED ID NOS: 166
SED ID NO 20
LENGTH: 250
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US-09-870-759-10
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Best Local S
Matches 123
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CURRENT APPLICATION UNBER: US/09/870,759

CURRENT FILING DATE: 2002-01-14

CURRENT FILING DATE: 2002-01-14
                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn version 3.1
SEQ ID NO 10
LENGTH: 266
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PRIOR FILING DATE: 2000-05-30
NUMBER OF SEQ ID NOS: 166
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| 180 KYLTDIKOLYTNOSKYETGYIKETPKINESEMPDFEPEPETOSKYLMIYKDIETLOSN 239
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                                                                                                                                                                  123;
                                                                                 11 ILIFALILVISTPHVLAESQPDPKPDELHKSSKFTGLMENMKVLYDDHHVSAINVKSIDQ
                    71 LRSHDLIYNVSGP---NYDKLKTELKNQEMATLFKDKNVDIYGVEYYHLCYLCENA---- 123
                                                                                                                       15 VLVTFLGLTIS-QEVFA--QQDPDPSQLHRSSLVKNL-QNIYFLYEGDPVTHENVKSVDQ 70
                                                                                                                                                                                          Similarity
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FLYFDLIYSIKDTKLGNYDNVRVEFKNKDLADKYKDKYVDVFGANYYYQCYFSKKINDIN 130
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83.7%; Pred. No. 7.56
tive 7; Mismatches
                                                                                                                                                                  43.6%; score 576.5; DB 9;
48.2%; Pred. No. 1.8e-43;
tive 38; Mismatches 75;
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I LENGTH: 239
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-09-150-947B-12
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                                                                                                                                                                                                                                  GENERAL INFORMATION
                                                                                                                                                                                                                                                  Sequence 8, Application US/10151336
Publication No. US20030079248A1
                                                  APPLICANT: Mason, Hugh
APPLICANT: Palmer, Kenneth
APPLICANT: Hefferon, Kathleen
APPLICANT: Hor, Teafrir
APPLICANT: Hor, Teafrir
TITLE OF INVENTION: Gemini Virus Vectors for Gene Expression
FILE REFERENCE: 4868/84453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 43.6%; Score 576; DB 10; Best Local Similarity 49.4%; Pred. No. 1.7e-43; Matches 117; Conservative 36; Mismatches 68
   CURRENT APPLICATION NUMBER: US/10/151,336
CURRENT FILING DATE: 2002-05-20
PRIOR APPLICATION NUMBER: US/09/414,276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: BROAD SPECTRUM PYROGENITY
TITLE OF INVENTION: BROAD SPECTRUM PYROGENITY
TITLE OF INVENTION: ANTAGONISTS AND VACCINES
FILE REPERENCE: A31557-PCT-USA-6
CURRENT FILTO: ANTAGONISTS AND VACCINES
CURRENT FILTO: ANTAGONISTS US/09/150, 947B
CURRENT FILTO: DATE: 1998-09-10
PRIOR APPLICATION NUMBER: PCT/IL97/00438
PRIOR FILTO: ANTE: 1997-12-30
PRIOR PILTO: ANTE: 1997-12-30
PRIOR PILTO: ANTE: 1997-12-30
PRIOR PILTO: ANTE: 1997-12-30
PRIOR APPLICATION NUMBER: ISBAEL 119938
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APPLICANT: Arad,
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                                                                                                                                                                                                                                                                                                                                                                                137 EGNHLEIPKKIVVKVSIDGIQSLSFDIETNKKWYTAQELDYKVRKYLTDNKQLYTNGPSK 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62 DNYRVEFKNKDLADKYKDKYVDVFGANYYYQCYFSKKTNDINSHETDKRKTCMYGGVTEH 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30 AQQDPDPSQLHRSSLVKNL-QNIYFLYEGDPVTHENVKSVDQLRSHDLIYNVSGP---NY 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 SQPDPKPDELHKSSKFTGLMENMKVLYDDNHVSAINVKSIDQFLYFDLIYSIKDTKLGNY 61
                                                                                                                                                                                                                                                                                                                                                                                                                         YETGYIKFIPKNKESEWEDEFPEP--EFTQSKYLMIYKDNETLDSNTSQIEVYLTTK 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NGNQLDKYRSITVRVFEDGKNLLSFDVQTNKKKVTAQELDYLTRHYLVKNKKLYEFNNSP 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LDSNTSQIEVYLTTK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FastSEQ for Windows Version 3.0
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NUMBER: US/09/414,276
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              68;
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                                                                                     in Plants
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APPLICANT: Ultich, Robert G.

TITLE OF INVENTION: Bacterial Superantigen Vaccines
FILE REFERENCE: 003/233/Sap (CHRENT ETLING DATE: 105/10/002/784A)
CURRENT FILING DATE: 105/11/26
CURRENT FILING DATE: 105/882,431; 09/144,776
FRIOR ALPLICATION NUMBER: 08/882,431; 09/144,776
FRIOR FILING DATE: 97-06-25; 98-09-01
NUMBER OF SEO ID NOS: 40
SEOTWARE: Apple Macintosh Microsoft Word 6.0
SEO ID NO 6
SEO ID NO 6
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US-10-002-784A-6
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                                                                                                                                                                                                                                                                           Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 6, Application US/10002784A Publication No. US20030036644A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 22
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 8
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR FILING DATE: 1999-10-07
                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 266
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                                                                                                                                                                                                                                                                        Local Similarity
     131
                                             124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181 KYTAQELDYLTRHYLVKNKKLYEFNNSPYETGYIKFI-ENENSFWYDMMPAPGDKFDQSK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 YFSKKTNDINSHQTDKRKTCMYGGVTEHNGNQLDKYRSITVRVFEDGKNLLSFDVQTNKK 180
                                                                                     71
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                                                                                                                                                            11 ILIFALILVISTPNVLAESQPDPKPDELHKSSKFTGLMEDMKVLYDDNHVSAINVKSIDQ
                                                                                                                                                                                                 15 VLVTFLGLTIS-QEVFA--QQDPDPSQLHRSSLVKNL-QNIYFLYEGDPVTHENVKSVDQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 SAINVKSIDGSLYFDLIYSIKDTKLGNYDNVRVEFKNKDLADKYKDKYVDVFGANYYYQC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 THENVKSVDQLRSHDLIYNVSGP---NYDKLKTELKNQEMATLFKDKNVDIYGVEYYHLC 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MDKRLFISHVILIFALILVISTPNVLAESOPDPKPDELHKSSKFTGLMENMKVLYDDNHV 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8 LKKMVFF----VLVTFLGLTIS-QEVFA--QQDPDPSQLHRSSLVKNL-QNIYFLYEGDPV 60
                                                                                                                 LRSHDLIYNVSGP---NYDKLKTELKNQEMATLFKDKNVDIYGVEYYHLCYLCENA----
SHQTDKRKTCMYGGVTEHNGNQLDKYRSITVRVFEDGKNLLSFDVQTNKKKVTAQELDYL
                         ----ERSACIYGGVTNHEGNHLEIPKKIVVKVSIDGIQSLSFDIETNKKMYTAQELDYK 178
                                                                               FLYFDLIYSIKDTKLGDYDNVRVEFKNKDLADKYKDKYVDVFGANYYYQCYFSKKTNDIN
                                                                                                                                                                                                                                                    Conservative
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                                                                                                                                                                                                                                            42.9%; Score 567.5; DB y;
47.5%; Pred. No. 1.1e-42;
47. Mismatches 75;
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US-10-002-784A-10
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                                                               NUMBER OF SEQ ID NOS: 40
SOFTWARE: Apple Macintosh Microsoft Word 6.0
SEQ ID NO 8
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                                                                                                                                                                                                                                                                                                                         Sequence 8, Application US/10002784A Publication No. US20030036644A1
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Best Local Similarity 48.5%;
Matches 115; Conservative 3
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SOFTWARE: Apple Macintosh Microsoft Word 6.0
SEQ ID 0 10
                                                                                                               APPLICANT: Ulrich, Robert G.
TITLE OF INVENTION: Bacterial Superantigen Vaccines
FILE REFERENCE: 003/23/SAP
CURRENT APPLICATION SUMBER: US/10/002,784A
CURRENT FILING DATE: 2001-11-26
PRIOR APPLICATION MUMBER: 08/88/31; 09/144,776
PRIOR APPLICATION MUMBER: 08/88/31; 09/144,776
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TITLE OF INVENTION: BACKETIA! Superantigen Vaccines
FILE REFERENCE: 003/233/Ssp.
CURRENT APPLICATION NUMBER: US/10/002/784A
CURRENT FILING DATE: 27001111-26
PRIOR APPLICATION NUMBER: 08/883,431: 09/144,776
PRIOR APPLICATION NUMBER: 08/883,431: 09/144,776
PRIOR FILING DATE: 97-06-23; 98-09-01
                     LENGTH: 266
TYPE: PRT
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ORGANISM: Artificial sequence
ORGANISM: Artificial sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NGNQLDKYRSITVRYFEDGKNLLSFDVQTNKKKVTAQELDYLTRHYLVKNKKLYEFNNSP
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Pred. No. 2.4e-42;
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; MOLECULE TYPE:
US-08-882-431-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Robert
                                                                                                                    TELEFAX: (301) 619-7714
INFORMATION FOR SEQ ID NO:
                                                                                                      SEQUENCE CHARACTERISTICS:
                                                                                                                                                    TELECOMMUNICATION INFORMATION: TELEPHONE: (301) 619-2065
                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Microsoft Word 6.0 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: Bacteria TITLE OF INVENTION: Vaccines NUMBER OF SEQUENCES: 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
                                                               TYPE:
                                                                                                                                                                                      NAME: Moran, John
REGISTRATION NUMBER: 26
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: John Moran
STREET: US Army MRMC CITY: FORT DETRICK
                                                     STRANDEDNESS:
                                                                                                                                                                                                                                                               FILING DATE:
                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.5
                                                                                                                                                                                                                                                                              APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER:
                                                                                  LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             191 TRHYLYKNKKLYEFUNSPYETGYIKFI-ENENSFWYDMAPAPGDKFDQSKYLLMAYNDNKM 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            124 ----ERSACIYGGVTNHBGNHLEIPKKIVVKVSIDGIQSLSFDIETNKKMVTAQELDYK 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11 ILIFALILVISTPNVLAESQPDPKPDELHKSSKFTGLMENMKVLYDDNHVSAINVKSIDQ 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15 VLVTFLGLTIS-QEVFA--QQDPDPSQLHRSSLVKNL-QNIYFLYEGDPVTHENVKSVDQ 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21702-5012
                                                                    Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SHOTDKRKTCMYGGVTEHNGNOLDKYRSITVRVFEDGKNLLSFDVQYNKKKVTAQELDYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FRYFDLIYSIKDTKLGNYDNVRVEFKNKDLADKYKDKYVDVFGANAYYQCAFSKKTNDIN 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MARYLAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VDSKDVKIEVYLTTK 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VRKYLTDNKQLYTNGPSKYETGYIKFIPKNKESFWFDFFPEP--EFTQSKYLMIYKDNET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                  Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sina Bavari
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mark A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Robert G. Ulrich,
Mark A. Olson
                                                                                                                                                                                                                                                                                                                                 June 25,
                                                   Unknown
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                                                                                                                                                                                                                                                                                                                                                  US/08/882,431
                                                                                                                                                                                                         26,313
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                38; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 558.5; DB Pred. No. 7e-42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Superantigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               В
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RESULT 14
US-08-882-431-14
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                                                                                         US-08-882-431-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 42.2%; Score 558; DB 1; Length 239
Best Local Similarity 47.7%; Pred No. 6.7e-42;
Matches 113; Conservative 39; Mismatches 69; Indels
     Matches 115;
                                                                                                                                                                                                                                    TELEFAX: (301) 619-7714
NFORMATION FOR SEQ ID NO:
                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.5
                                                                                                                                                                                                                                                                          NAME: MOZAN, John
REGISTRATION NUMBER: 26,313
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 619-2065
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Microsoft Word 6.0 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: Bacterial Superantigen TITLE OF INVENTION: Vaccines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Mark A. Olson APPLICANT: Sina Bavari
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
                                                                                                             MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                            TYPE: Amino Acid
STRANDEDNESS: Uni
TOPOLOGY: Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US FILING DATE: June 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: USAMY MEMC-504 Scott Street MCMR-JA (John Moran-Patent Atty)
CITY: FORT DETRICK
                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       122 NGNQLDKYRSITVRVFEDGKNLLSFDVQTNKKKVTAQELDYLTRHYLVKDKKLYEFNNSP 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        62 DNVRVEFKNKDLADKYKDKYVDVFGANAYYQCAFSKKTNDINSHQTDKRKTCMYGGVTEH 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30 AQQDPDPSQLHRSS-LVKNLQNIYFLYEGDPVTHENVKSVDQLRSHDLIYNVSGP---NY 85
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EGNHLEIPKKIVVKVSIDGIQSLSFDIETNKKWYTAQELDYKVRKYLTDNKQLYTNGPSK 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SQPDPKPDELHKSSKFTGKMENMKVLYDDNHVSAINVKSIDQFRYFDLIYSIKDTKLGNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MARYLAND
     Conservative
                                                                                                                               Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Robert G. Ulrich,
                                                                                                           Peptide
                                                                                                                                                   Unknown
41.8%; score 553; DB 1; Length 266; 44.9%; pred. No. 2.2e-41; tive 51; Mismatches 72; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US/08/882,431
     18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16;
     Gaps
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US-10-002-784A-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 40
SOFTWARE: Apple MacIntosh Microsoft Word 6.0
SEQ ID NO 14
LENGTH: 266
                                                                                                                                                                                                                                                                                                                                                                      Matches 115;
                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: ULTICH, Robert G.
TITLE DE INVENTON: Batchella Superantigen Vaccines
FILE REFERENCE: 003/33/584P
CURRENT APPLICATION (NUMBER: US/10/002,784A
CURRENT FILING DATE: 2001-11-26
PRIOR APPLICATION (NUMBER: 05/88),431; 09/144,776
PRIOR APPLICATION (NUMBER: 05/0-25; 98-09-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Artificial sequence FEATURE:
                                                                          189
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                                                                                               178 KVRKYLTDNKQLYTNGPSKYETGYIKFIPKNKESFWFDFFPEP--EFTQSKYLMIYKDNE
                                                                                                                                                                                       124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          129 GKVTGGKTCMYGGITKHEGNHFDNGNLQNVLIRVYENKRNTISFEVQTDKKSVTAQELDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            124 ER----SACIYGGVTNHEGNHLEIP--KKIVVKVSIDGIQSLSFDIETNKKMYTAQELDY 177
249
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12 LIFALILVLETPNVLAE---SQPDPTPDELHKASKFTGLMENMKVLYDDHYVSATKVKSV
                                                                                                                                                                                                                                                                                                                  11 MVF-FYLVTFLGLTISQEVFAQQDDDDSQLHRSSLVKNL-QNIYFLYEGDPVTHENVKSV 68
                                                                                                                                                                                                                                                                                              12 LIFALILVLFTPNVLAE---SQPDPTPDELHKASKFTGLMENMKVLYDDHYVSATKVKSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DQLRSHDLIYNVSG---PNYDKLKTELKNQEWATLFKDKNVDIYGVEYYHLCYLC--ENA 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TVDSKSVKIEVHLTTK
                                 TLDSNTSQIEVYLTTK 251
                                                                        KARNELINKKNLYEFNSSFYETGYIKFIENNGNTFWYDMMPAPGDKFDQSKYLMMYNDNK
                                                                                                                                                GKYTGGKTCMYGGITKHEGNHFDNGNLQNYLIRVYENKRNTISFEVQTDKKSYTAQELDI 188
                                                                                                                                                                                 ER----SACIYGGVTNHEGNHLEIP--KKIVVKVSIDGIQSLSFDIETNKKMVTAQELDY 177
                                                                                                                                                                                                                        DKFRAHDLIYNISDKKLKNYDKVKTELLNEGLAKKYKDEVVDVYGSNYYVNCYFSSKDNV 128
                                                                                                                                                                                                                                                          DQLRSHDLIYNVSG---PNYDKLKTELKNQEMATLFKDKNVDIYGVEYYHLCYLC--ENA 123
                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                     41.8%;
  264
                                                                                                                                                                                                                                                                                                                                                                      51; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                     Score 553; DB 9; Length 266; Pred. No. 2.2e-41;
                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                        18;
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                                                                             248
                                                                                                              235
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Search completed: June 23, 2003, 16:16:38 Job time: 13.9166 secs

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11 MVF-FVLVTFLGLTISQEVFAQQDPDPSQLHRSSLVKNL-QNIYFLYEGDPVTHENVKSV 68

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Minimum DB
Maximum DB
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                                                                                    Post-processing: Minimum Match 0%
Maximum Match 10
Listing first 45
                                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                         Sequence:
                                                                                                                                                                                                                                                                                                                                         Title:
Perfect score:
                                                                                                                                                                                                                                         Searched:
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                                                                                                                                                                                                                                                                                                                                                                                                                               Run on:
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                                                                                                                                                     seq length: 0
seq length: 2000000000
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Gapop 10.0 , Gapext 0.
                                                                                                                                                                                                                                       283224 seqs, 96134422 residues
                                                                                                                                                                                                                                                                                                                                                                                                                             June 23,
                                                                                                                                                                                                                                                                                                                                                            US-10-002-784A-16
                                                   PIR_73:*
                                                                                                                                                                                                                                                                                                                         MENNKKYLKKMVFFVLVTFL......KDNETLDSNTSQIEVYLTTK 25:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GenCore version
Copyright (c) 1993 - 2003
pir1:*
pir2:*
pir3:*
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1304.163 Million cell updates/sec
                                                                                 45 summaries
                                                                                                      100%
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. the total score distribution

SUMMARIES

29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	٠	8	7	o	. UT	4	w	2	1		Result
111	111	114	114	125	128	129.5	174	211	251.5	264	305.5	307	308	311.5	336	337	338	340	481	548	549	551.5	576.5	1075.5	1109	1234	1239	1315	OCOLO	
8.4	8.4	8.6	8.6	9.5	9.7	9.8	13.2	16.0	19.0	20.0	23.1	23.2	23.3	23.6	25.4	25.5	25.6	25.7	36.4	41.5	41.5	41.7	43.6	81.4	83.9	93.3	93.7	99.5	March	
292	234	234	232	227	157	231	133	235	242	239	240	257	257	258	260	136	260	258	258	266	266	266	266	250	236	236	236	251	Tenden	
2	N	N	N	N	N	N	ν	N	N	N	N	N	N	N	ν	Ņ	N	N	N	ш	N	N	ш	_	N	N	N	۲		3
в89807	в89992	C89807	F89807	C89808	A89942	D89807	в89969	A30509	C89969	D89969	G89991	A28664	A28179	н89968	C89984	A89969	E89969	A33953	G89968	ENSAC1	A60114	S11885	ENSAB6	A26152 .	S18789	S18786	S18783	S29659	15	;
_	ock s	10	13	_	ical		enterotoxin Yentl	exotoxin C precurs	extracellular ente	enterotoxin SEM [i	a r	×		Se			ည	U	ar en	C-1	C-2 p	G	-	õ	A precu	type A	type A		Description	,

4 4	3	42	41	40	39	38	37	36	35	34	မှ	32	31	30
103.5	103.5	104.5	104.5	105	105	105	105	105.5	108	108	108.5	108.5	109	109.5
7.8	7.8	7.9	7.9	7.9	7.9	7.9	7.9	8.0	8.2	8.2	8.2	8.2	8.2	8.3
235	241	1856	1367	894	840	824	770	1790	493	434	596	231	234	825
20 6	N	N	N	N	N	N	N	N	N	N	N	N	_	N
C97252	B8988	C95008	T18466	137282	137281	A48910	B48910	S67593	G90604	T28342	E96935	н89806	XCSAS1	H82885
prrC protein - Esc probable membrane	hypothetical prote	immunoglobulin Al	hypothetical prote	Dsclb precursor -	Dscla precursor -	desmocollin la pre	desmocollin lb pre	transport protein	hypothetical prote	ORF MSV181 hypothe	FUSION, methionine	exotoxin 7 (import	toxic shock syndro	hypothetical prote

ALIGNMENTS

A.Status: nucleic acid sequence not shown; translation not shown A.Molecule type: DNA.A.Molecule type: DNA.A.Molecule type: DNA.A.Molecule type: DNA.A.Molecule type: DNA.A.Molecule type: DNA.Molecule typ R. Nelson, K.; Schlievert, P.M.; Selander, R.K.; Musser, J.M.
J. Exp. Ned. 174, 1271-1274, 1991
A.Fitile: Characterization and clonal distribution of four alleles of the spea gene en
A. Reference number: S18782; MJID:92044323; PMID:1940804
A. Accession: \$18782 exotoxin type A precursor (allele 1) - Streptococcus pyogenes phage 712
N.Alternate names: erythrogenic toxin; scarlet fever toxin
C.Species: Streptococcus pyogenes phage 712
C.Date: 10-Sep 1999 #sequence_rvision 10-52
C.Date: 10-Sep 1999 #sequence_rvision 70-52
C.Accession: S29659; S18782; S18784; S18785; S18791; S18796; S18797; S18800 A; resolutes: 7 449 Note: A; resolutes: 7 449 Note: A; resolutes: 7 449 Note: A; Ross-references: EMELX: X61560; NID:947287; PIDN:CAA43758.1; PID:947288 A; Experimental source: Streptococcus pyogenes strain MGAS156 isolate Nebraska unassig A; Note: the nucleotide sequence was submitted to the EMBL Data Library, September 199 A; Molecule type: DNA A; Residues: 1-251 <WEE> A;Title: Nucleotide sequence of the type A streptococcal exotoxin (erythrogenic toxin A;Reference number: S29659; MUID:86166804; PMID:3514452 A;Cross-references: GB:U40453; EMBL:M19350; NID:g1877426; PIDN:AAC48868.1; R;Nelson, K.; Schlievert, P.M.; Selander, R.K.; Musser, J.M. A; Accession: S29659 Infect. Immun. 52, 144-150, 1986 R; Weeks, C.R.; Ferretti, PID: 918774

A; Accession: S18784

A; Status: nucleic acid sequence not shown; translation not shown A; Molecule type: DNA A; Residues: 9-244 <NEA>

A; Experimental source: Streptococcus pyogenes A; Note: the nucleotide sequence was submitted A; Accession: \$18785 A:Cross-references: PMBL:X61556, NID:947291, PINN:CAA4754.1, PID:977292 A:Experimental source: Streptococcus pyogenes strain McAS165 isolate Minnesota unassi A:Note: the nucleotide sequence was submitted to the EMBL Data Library, September 199

A; Oross: references: EMBL:X61559; NID:47293; PIDN:CAA4757.1; PID:947294
A; Experimental source: Streptococcus pyogenes strain mAXS167 isolate Texas unassigned
A; Note: the nucleotide sequence was submitted to the EMBL Data Library, September 199 A; Status: nucleic acid sequence not shown; translation not shown A; Molecule type: DNA A; Residues: 9-244 (NEZ) A; Accession: S18791

A; Status: nucleic acid sequence not shown; translation not shown

A; Molecule type: DNA A; Residues: 9-244 <NEY>

A:Cross:references: EMBL:X61555; NID:g47309; PIDN:CAA4753,1; PDD:g47310
A:Cross:references: EMBL:X61555; NID:g47309; PIDN:CAA4753,1; PDD:g47310
A:Experimental source: Streptococcus pyogenes strain Mak3237 isolate Arizona unassign
A:Mote: the nucleocide sequence was submitted to the EMBL Data Library, September 199

A; Molecule type: DNA A; Residues: 9-244 <NEO> A;Status: nucleic A; Accession: S18796 acid sequence not shown; translation not shown

A;Cross-references: EMBL:X61557; NID:g47319; PIDN:CAA43755.1; PID:g47320

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A; Experimental source
A; Note: the nucleotic
A; Accession: $18797
A; Status: nucleic ac
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J. Exp. Med. 174, 1791. 1734, 199 Schinder, R.K.; Musser, J.M.
M.Title. Characterization and clonal distribution of four alleles
A. Reference number: $18782; MUID:92044323; PMID:1940804
A. Recession: $12782.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          exotoxin type A preoursor (allele 3) - Streptococcus pyogenes phage (strain MG) N.Alternate names: scarlet fever toxin ("Species: Streptococcus pyogenes phage ("Species: Streptococcus pyogenes phage A.Variety: strain MGAS198 isolate Nebraska; strain MGAS485 isolate Yugoslavia; C;bate: 29-Jan-1993 *Bequence_revision 29-Jan-1993 *text_change 16-Jul-1999 C;Accession: S10738; S10739; S10734; S10801; S10798; S10794; S10010; S10798; S10794; S10010; S10798; S10794; S10010; S10794; S10794;
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                                                                                                                                                                                                               A; Cross references: EMBL:X61588; NID:947289; PIDN:CAA4376.1; PID:947280
A; Experimental source; Etrain MAS:158 isolate Nebraska unassigned phageo
A; Note: the nucleoxide sequence was submitted to the EMBL Data Library,
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C;Superfamily: enterotoxin B
C;Keywords: exotoxin
F;1-30/Domain: signal sequen
F;31-251/Product: exotoxin t;
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A;Experimental source: Streptococcus pyogenes strain MGAS500 isolate New Zemland unassi
A;Mote: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
C;Genetics:
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A;Experimental source: Streptococcus pyogenes strain NGAS94 isolate France unassigned A;Note: the nucleatide sequence was submitted to the EMBL Data Library, September 1991
A;Accession: $18800
A;Status; nucleic_scid sequence not shown; translation not shown
A;Cross-references: EMBL:X61569; NID:g47313; PIDN:CAA43767.1; PID:g47314
A;Experimental source: strain MGAS485 isolate Yugoslavia unassigned phage
                                                                                A; Molecule type: DNA
A; Residues: 1-236 <NEA>
                                                                                                                                                  A; Status: nucleic acid sequence not shown; translation not
                                                                                                                                                                                          A; Accession: S18793
                                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-236 <NEL>
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A; Residues: 9-228 <NES>
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A; Residues: 9-244 <NEH>
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1-30/Domain: signal sequence
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KYLTDAKOLYTNGSSKYETGYIKFIEKANESSFAEDEFPEEETGSKYLMIYKDAETLDSA 240
KYLTDAKOLYTNGPSKYETGYIKFIEKANESSFAEDEFPEEETTGSKYLMIYKDAETLDSA 240
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Pred. No. 1
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A:Note: the nucleotide sequence was submitted to the EMBL Data Library, September a:Accession: S18794
A; Status: nucleic acid sequence not shown; translation not shown
                                                                         199
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A; Molecule type: DNA A; Residues: 1-236 <N

236 <NEZ>

A; Note: the nucleotide sequence was A; Accession: S18801 A; Status: nucleic acid sequence not shown; translation not shown A;Cross-references: EMBL:X61570; NID:947315; PIDN:CAA43768.1; PID:947316 A;Experimental source: strain MGAS491 isolate United Kingdom unassigned submitted ç the EMBL Data Library, phage September 199

A; Molecule type: DNA A; Residues: 1-236 <NEY>

A;Status: nucleic A; Note: the nucleotide sequence was submitted A; Accession: S18798 A;Cross-references: EMBL:X61572; NID:g47333; PIDN:CAA43770.1; PID:g47334 A;Experimental source: strain MGAS624 isolate Germany unassigned phage acid sequence not shown; translation not shown ç the EMBL Data Library, September

A; Molecule type: DNA A; Residues: 1-236 <NEO>

A.Cross-references: EMEL:X61571; NID:407323; PIDN:CAA437691; PID:94734A A.Experimental source: Strain MGAS495 Isolate Germany unassigned phage A:Mote: the nucleotide sequence was submitted to the EMBL Data Library, September

A; Note: the nucleotide sequence was submitted C; Genetics: A; Gene: speA3

C;Superfamily: enterotoxin B
C;Keywords: exotoxin
C;Keywords: exotoxin
F;1-22/Domain: signal sequence (fragment) *status predicted
F;1-23/Domain: signal sequence (fragment) *status predicted Query Match Best Local Local Similarity 93.7%; Score 1239; Pred. No. 4 9; DB 2; 4.8e-85; predicted <SIG> Length 236;

9 KKMVFFVLVTFLGLTISQEVFAQQDPDPSQLHRSSLVKNLQNIYFLYEGDPVTHENVKSV Conservative Mismatches Indels 0 Gaps

129 61 69 IYGGVTNHEGNHLEIPKKIVYKVSIDGIQSLSFDIETNKKMYTAQELDYKVRKYLTDNKQ DQLLSHDLIYNVSGPNYDKLKTELKNQEMATLFKDKNIDIYGVEYYHLCYLCENAERSAC DQLRSHDLIYNVSGPNYDKLKTELKNQEMATLFKDKNVDIYGVEYYHLCYLCENAERSAC KKMVFFVLVTFLGLTISQEVFAQQDPDPSQLHRSSLVKNLQNIYFLYEGDPVTHENVKSV 120 128 60

181 189 LYTNGPSKYETGYIKFIPKNKESFWFDFFPEPEFTQSKYLMIYKDNETLDSNTSQI LYTNGPSKYETGYIKFIPKNKESFWFDFFPEPEFTQSKYLMIYKDNETLDSNTSQI 244

IYGGVTNHEGNHLEIPKKIVVKVSIDGIQSLSFDIETNKKMVTAQELDYKVRKYLTDNKQ

180

MGAS250

exotoxin type A precursor (allele 2) - Streptococcus pyogenes phage (strain MGAS; NALternate names: scarlet fever toxin (.Species: Streptococcus pyogenes phage (.Strain MGAS250) isolate for the property of the property of

gene

eμ

A;Status: nucleic acid sequence not shown; translation not shown

A; Molecule type: DNA
A; Residues: 1236 < NLD.
A; Residues: 1236 < NLD.
A; Cross-references: EMBL:x61561; NID:947297; PIDN:CAA43759.1; PID:947298
A; Experimental source: strain MCAS550 isolate California unassigned phage
A; Note: the nucleotide sequence was submitted to the EMBL Data Library, SG
A; Accession: S18787
A; Status: nucleic acid sequence not shown; translation not shown
A; Molecule type: DNA September

en

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A. Accession: S18799
A. Coross: references: EMEL:x61567; NID:g47325; PIDN:CAA43765.1; PID:g47326
A. Experimental source: strain MGA5496 isolate Germany unassigned phage
A: Note: the nucleotide sequence was submitted to the EMBL Data Library,
C:Genetics:
A. Gene: speA2
C:Superfamily: enterotoxin B
C:Keywords: exotoxin
F.11-22/Jonani: Signal sequence (fragment) #status predicted <NAT>
F.13-2356/Product: exotoxin type A (fragment) #status predicted <NAT>
F.13-2356/Product: exotoxin type A (fragment) #status predicted <NAT>
RESULT 4
Sla789
exotoxin A precursor (allele 4) - Streptococcus
whiternate names: scarlet fever toxin
C;Species: Streptococcus pyogenes
A; Variety: strain MGAS262 isolate California
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A:Cross-references: EMBL:X61566; NID:947317; PIDN:CAM43764.1, PID:947318

A:Note: the nucleotide sequence was submitted to the EMBL Data Library,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A:Cross:references: EML:X61565, NID:407311, PIDN:CAA43763.1, PID:947312
A:Experimental source: Extain MG3460 isolate Yugoslavia unassigned phage
A:More: the nucleotide sequence was submitted to the EMBL Data Library, September
A:Accession: 518795
A:Status: nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A:Cross: references: EMBL:X61564, NID:44705; PIDN:CAA43f62.1, PID:947306
A:Experimental source: Etrain MGAS285 isolate Colorado unassigned phage
A:Mote: the nucleotide sequence was submitted to the EMBL Data Library,
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A;XXPE:Imental source: Strain MGAS256 isolate California unassigned phage
A;XXPE: the nucleotide sequence was submitted to the EMBL Data Library, September
A;XCcession: S18790
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A:Residues: 1-236 (NEA)
A:Cross-references: EMEL:X61562; NID:947299; PIDN:CAA43760.1; PID:947300
A:Experimental source: Extrain MGAS251 isolate California unassignd phage
A:Rote: the nucleotide sequence was submitted to the EMBL Data Library, i
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A; Status: nucleic a
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A; Residues: 1-236 <NEZ>
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Best Local 9
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Residues: 1-236 <NEO>
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Pred. No. 1.1e-84;
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A26152
Streptococcal pyrogenic exotoxin type A precursor - Streptococcus Fittenate names: scarlet fever toxin; SPE type A (speA)
C;Species: Streptococcus sp.
C;Species: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10
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A; Residues: 1-250 <JOH>
C; Superfamily: enterotoxin
C; Keywords: exotoxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R.Johnson, L.P.; L'Italien, J.J.; Schlievert, P.M.
Mol. Gen. Genet. 203, 354-356, 1986
A.Title: Streptococcal pyrogenic exotoxin type A (scarlet A;Reference number: A26152; MUID:86284313; PMID:3526093
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121 ENAERSACIYGGVTNHEGNHLEIPKKIVVKVSIDGIQSLSFDIETNKKMVTAQELDYKVR 180

ENAERSACLYGGVTNHEGNHLEIPKKIVVKVSIDGIQSLSFDIEQIKN-GNCSRISYTVR

61 THENVKSVDQLRSHDLIYNVSGPNYDKLKTELKNQEMATLFKDKNVDIYGVEYYHLCYLC

120

60

120

MENNKEYLKKMYFFYLMKFLGLTILPKGICSTRPKPSQLQRSNLVKTFKIYIFFMRYTLV MENNKKYLKKMYFFYLYTFLGLTISQEYFAQQDPDPSQLHRSSLYKNLQNIYFLYEGDPY

THENVKSVDQLLSHDLIYNVSGPNYDKLKTELKNQEMATLFKDKNVDIYGVEYYHLCYLC

61

210;

Conservative

Similarity

81.4%; 83.7%;

Score 1075.5; DB 1; Pred. No. 7.5e-73; 7; Mismatches 33;

Length

250;

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Gaps

B

#text_change 10-Sep-1999

fever toxin) is related

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C;Date: 29-Jan-1993 #sequence_revision 29-Jan-1993 #t
C;Accession; Si9789
R;Nelson, K.; Schlievert, P.M.; Selander, R.K.; Musse
Exp. Med. 114, 1271-1274, 1991
A;Title: Characterization and clonal distribution of
A;Reference number: Si9782; MUID:92044323; PMID:19408
A;Recession: Si8789
A;Status: nucleic acid sequence not shown; translatic
                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: DNA
A; Residues: 1-236 <NEL>
A; Cross references: EMBL: X61573;
A; Note: the nucleotide sequence w
C; Centics:
A; Gene: SpeA
                                                                                                                                                                                                                                                                                                                                                     F;1-22/Domain: signal sequence (fragment) #status predicted <SIG>F;23-236/Product: exotoxin A (fragment) #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                          C; Keywords: exotoxin
                                                                                                                                                                                                                                                                                                                                                                                                              C; Superfamily: enterotoxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Date: 29-Jan-1993 #sequence_revision 29-Jan-1993 #text_change
                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                          Local 209;
                                                                121 IYGGVTNHEGNHLEIPKNILVKVSIDGIQSLSFDIETSKKMVTAQELDYKVRKHLTDNKQ
  181
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                 LYTNGPSKYETGYIKFIPKNKESFWFDFFPEPEFTQSKYLMIYKDNETLDSNTSQI
LYTNGPSKYETGYIKFISKDKETFWFDFFPEPEFNQVKYLMIYKDNETLDSSTSQI
                                                                                         IYGGVTNHEGNHLEIPKKIVVKVSIDGIQSLSFDIETNKKMVTAQELDYKVRKYLTDNKQ
                                                                                                                                           DQLLSHDLIYNVSGLNYDKLKTELKNREMSTLFKNKNVDIYGVEYYYHCYLCRNAKRRAC
                                                                                                                                                            DOLRSHDLIYNVSGPNYDKLKTELKNQEMATLFKDKNVDLIYGVEYYHLCYLCENAERSAC
                                                                                                                                                                                                              KKMYFFYLYTFLGLTISQEYFAQQDPDPSQLHRSSLYKNLQNIYFLYEGDPYTHENYKSY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NID:g47303; PIDN:CAA43771.1; PID:g47304
                                                                                                                                                                                                                                                                                                      Score 1109;
Pred. No. 2.
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2.3e-75;
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RESULT 6

ENSAB6

anterotoxin B precursor - Staphylococcus aureus
C.Specias: Staphylococcus aureus
R.Jones: C.J., Khan, S.A.
J. Bacteriol. 166, 29-33, 1986
A.Ttle: Nucleotide sequence of the enterotoxin B gene from Staphylococcus aureus
A.Reference number: S27360; MUID:86168029; PMID:3957869
A.Rocession: S27360
A.Molecule type: DNA
A.Reference number: S27360 AND A.Reference numb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ribung T.Y. Bergdoll, M.S.
J. Blol. Chem. 245 3511-517, 1970

A;Iltle: The primary structure of staphylococcal enterotoxin B.
A;Reference number: A25064 MUID:71007901; PMID:5470820

A;Contents: annotation; clymotryptic peptides
R;Huang, I.Y.; Bergdoll, M.S.
J. Blol. Chem. 245 3493-3510, 1970

A;Title: The primary structure of staphylococcal enterotoxin B.
A;Reference number: A36063, WUID:71007900; PMID:5470819

A;Reference number: A3063, WUID:71007900; PMID:5470819

A;Contents: annotation; tryptic peptides
R;Schantz, E.J.; Roessler M.G.; Wagman, J.; Spero, L.; Dunnery,
Biochamistry 4 1011-1016, 1965
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A:Molecule type: protein
A:Molecule type: protein
A:Experimental source: strain S-6
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C:Keywords: enterotoxin; extracellular protein; toxin
F:1=37/Domain: signal sequence #status predicted <SIG>
F:28-266/Product: enterotoxin B #status experimental <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A.Title: Identification of functionally active fragments of staphylococcal enterotoxin
A;Reference number: S27240; MUID:93049338; PMID:1425690
A;Accession: S27240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A.Title: Purification of staphylococcal enterotoxin B. A.Title: Purification of staphylococcal enterotoxin B. A.Reference number: A99848; MUID:66035792; PMID:4953518. A.Contents: annotation, biological source of protein R.Alakhov, V.Y., Klinsky, E.Y., Klosov, H.I.; Mourer-Fr. Bur. J. Biochem. 209, 033-828; 1992
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R:Hunng, I.Y.; Bergdoll, M.S.
J. Blol. Chem. 245, 3318-3325, 1970
A:Title: The primary structure of staphylococcal enterotoxin A:Reference number: A92065; MUID:71007902; PMID:5470821
A;Accession: A92065
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A;Experimental source: strain S6
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124 ----ERSACIYGGVTNHEGNHLEIPKKIVVKVSIDGIQSLSFDIETNKKMVTAQELDYK 178
                                                               71 FLYFDLIYSIKDTKLGNYDNVRVEFKNKDLADKYKDKYVDVFGANYYYQCYFSKKTNDIN 130
                                                                                                                                        71
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                                                                                                                         LRSHDLIYNVSGP---NYDKLKTELKNQEMATLFKDKNVDIYGVEYYHLCYLCENA---- 123
                                                                                                                                                                                                            ILIFALILVISTPNVLAESQPDPKPDELHKSSKFTGLMENMKVLYDDNHVSAINVKSIDQ 70
                                                                                                                                                                                                                                                                           VLVTFLGLTIS-QEVFA--QQDPDPSQLHRSSLVKNL-QNIYFLYEGDPVTHENVKSVDQ 70
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                                                                                                                                                                                                                                                                                                                                                                                      43.6%;
                                                                                                                                                                                                                                                                                                                                                                                 Score 576.5; DB 1
Pred. No. 1.1e-35;
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                                                                                                                                                                                                                                              Maurer-Fogy,
                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                   Length 266;
                                                                                                                                                                                                                                                                                                                                                    Indels
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S
                        A; Molecule type: DNA
A; Residues: 1-266 <BOH>
A; Accession: B60114
A; Molecule type: protein
A; Residues: 28-66 <BOH2>
                                                                                                                                                                                        CiSpecies: Staphylococcus aureus
CiSpecies: 10.Nov-1992 *Sequence_revision 10.Nov-1992 *ftext_change 16.Jul-1999
Cipatression: A60114, B60114, 33866
R;Bohboch, GA, Schilsvert, P.M.
Infect. Immun. 57, 2249-2527, 1989
A;Fittle: Commervation of the biologically active portions of staphylococcal enterotox A;Reference number: A60114; NUID:89277549; PMID:2543637
A;Accession: A6014
A;Schilary active portions of the biologically active portions of staphylococcal enterotox A;Reference number: A60114; NUID:89277549; PMID:2543637
A;Accession: A6014
A;Schilary active portions of the biologically active portions of staphylococcal enterotox A;Reference number: A60114; NUID:89277549; PMID:2543637
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A; Residues: 1-266 <HOV>
A; Cross-references: 6B:X51661; NID:g46570; PIDN:CAA35972.1; PID:g46571
C; Superfamily: enterotoxin B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOI. Gen. Genet. 220, 329-333, 1990.
N.Title: Nucleotide seguence of the stabhylococcal enterotoxin C3
N.Reference number: S11885; MUID:90220508; PMID:2325627
N.Accession: S11885
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 enterotoxin C3 - Staphylococcus aureus C;Specles: Staphylococcus aureus C;Date: 19-Mar-1997 tsequence_revision 19-Mar-1997 C;Accession: S11885
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           enterotoxin C-2 precursor - Staphylococcus aureus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N; Alternate names: enterotoxin C-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      131
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         238 DSNTSQIEVYLTTK 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              71
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FLAHDLIYNISDKKLKNYDKVKTELLNEDLAKKYKDEVVDVYGSNYYVNCYFSSKDNVGK 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LRSHDLIYNVSG---PNYDKLKTELKNQEMATLFKDKNVDIYGVEYYHLCYLC--ENAER 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SHQTDKRKTCMYGGVTEHNGNQLDKYRSITVRVFEDGKNLLSFDVQTNKKKVTAQELDYL 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RNFLINKKNLYEFNSSPYETGYIKFIENNGNTFWYDMMPAPGDKFDQSKYLMMYNDNKTV 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VTGGKTCMYGGITKHEGNHFDNGNLQNVLVRVYENKRNTISFEVQTDKKSVTAQELDIKA 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VDSKDVKIEVYLTTK 264
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DSKSVKIEVHLTTK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ----SACIYGGYTNHEGNHLEIP--KKIYVKVSIDGIQSLSFDIETNKKMYTAQELDYKV 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ILIFALILVISTPNVLAESQPDPMPDDLHKSSEFTGTMGNMKYLYDDHYVSATKVKSVDK
Betley, M.J
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Gaps

70

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J. Bacteriol. 171, 4507-4510, 1989
A:Title: Nucleotide sequence of the type C-3 staphylococcal enterotoxin gene suggests A; Beference number: A33866; MUID:89327174; PMID:2473979
A; Accession: A3386
A; Status: perlaining:
A; Status: perlaining:
A; Molecule type: DNA
A; Molecule type: DNA
A; Rosidues: 1,265 < COUP
A; Cross-references: GB:M28364; NID:g153003; PIDN:ANA26624.1; PID:g153004
A; Generics: GB:M28364; NID:g153003; PIDN:ANA26624.1; PID:g153004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ENSACI :

enterotoxin C-1 precursor - Staphylococcus aureus

c;species: Staphylococcus aureus

c;species: 5-Nov-1984 *soquence_revision 05-Jan-1996 *text_change 18-Jun-1999

c;baccesion: s06356; A01816

R;sobacch G-1, Schilererit, P-M.

R;sobacch G-1, Schilererit, P-M.

A;rettie: Nocleocide sequence of the staphylococcal enterotoxin Cl gene and 1

A;rettie: Nocleocide sequence of the staphylococcal enterotoxin Cl gene and 1

A;Reference number: 806356; MUID:88038552; PMID:2823067
                                                                                                                                                                                                                                                                                                                         R;Schmidt, J.J.: Spero, L.
J. Blol. (Dhen. 258, 6300-6306, 1983
J. Blol. (Dhen. 258, 6300-6306, 1983
A;Title: The complete amino acid sequence of Staphylococcal enterotoxin
A;Reference number: A01816, MUID:83213327; PMID:6189824
A;Accession: A01816
A;Accession: A01816
A;Accession: A01816
A;Bolecule type: protein
A;Besidues: 28-75; 'IL',78-176,'N',178-266 <SCH>
C;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: DNA
A; Residues: 1-266 < BOH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Accession: S06356
                                                                                                                                                F;28-266/Product: enterotoxin C-1 *scarus experimental F;120-137/Disulfide bonds: *status experimental
                                                                                                                                                                                C:Superfamily: enterotoxin B
C:Keywords: enterotoxin
F:1-27/Domain: signal sequence #status predicted <SIG>F:1-27/Domain: signal sequence #status experimental
F:28-266/Product: enterotoxin C-1 #status experimental
                                                                                                                                                                                                                                                                                                     A;Gene: entCl
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                                                                                                Query Match
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                                                                        Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DKFLAHDLIYNISDKKLKNYDKVKTELLNEDLAKKYKDEVVDVYGSNYYVNCYFSSKDNV 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TLDSNTSQIEVYLTTK 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KARNFLINKKNLYEFNSSPYETGYIKFIENNGNTFWYDMAPAPGDKFDQSKYLMMYNDNK
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Pred. No. 1
                                                Score 548; DB 1; I
pred. No. 1.4e-33;
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                                                                                                    Length 266;
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enterotoxin D precursor - Staphylococcus aureus
C;Specias: Staphylococcus aureus
C;Specias: Staphylococcus aureus
C;btec: 09-Mar-1990 #text_change 15-Oct-1999
C;Accession: A33953
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11 MVF-FVLVTFLGLTISQEVFAQQDPDPSQLHRSSLVKNL-QNIYFLYEGDPVTHENVKSV

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R;Ruroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K. Lancet 357, 125-1240, 2001
A;Fithe: Whole genome sequencing of meticillin-resistant Stapylococcus aureus. A;Riche: Whole genome sequencing of meticillin-resistant Stapylococcus aureus. A;Reference number: A89758; MJID:21311952; PMID:11418146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         extracellular enterotoxin type G precursor [imported] - Staphylococcus aureus (strain c.species: Staphylococcus aureus c.pate: 10-May-2001 #text_change 22-Oct-2001 c.pate: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001 c.pates: 10-May-2001 m.pates: 10-May-2001 m.pat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross:references: GB:BA000018; PID:g13701617; PIDN:BAB42910.1; GSPDB:GN00149
A;Experimental source: strain N315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            G89968
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-258 < KUR>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12
                                                                                                                                                                                                          176 DYKYRKYLTDNKOLYYNGDSKYETGYIKFIPKNKESFWFDFPFPEPE---FTQSKYLMIYK 232
                                                                                                                                                                                                                                                                                                                                        121
                                                                                                                                                                                                                                                                                                                                                                                       122 NAE-----RSACIYGGYTNHEGNHLEIPKKIVVKVSIDGIQSLSFDIETNKKMYTAOEL 175
240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62 HENVKSVDQLRSHDLIYNVSGPNYDKLKTELKNQEMATLFKDKNVDIYGVEYYHLCYLCE 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MKKLSTVIIILILEIVFHNMNYVNAQPDPKLDELNKVSDYKNNKGTMGNVMNLYTSPPVE 60
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                                                                                                                                                                                                                                                                                                                                        SEPDINQNFGGCCMYGGLTFNSSEN-ERDKLITVQVTIDNRQSLGFTITTNKNMVTIQEL
                                                                                                                                                                 DYKARHWLTKEKKLYEFDGSAFESGYIKFTEKNNTSFWFDLFPKKELVPFVPYKFLNIYG
DNKVVDSKSIKMEVFLNT
                                                                                   DNETLDSNTSQIEVYLTT
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           257
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Pred. No. 1.3e-28;
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A:Status; preliningy
A:Molecule type, DNA
A:Residues; I1-260 - KURD-
A:Cross-references; GB:BA000018; PID:913701623; PIDN:BAB42916.1; GSPDB:GN00149
A:Experimental Source: Strain W315
C:Genetics:
A:Gene: Seo
                                                                                                                                                                                                                                                                                                                                                                                                                                                   enterotoxin Seo [imported] - Staphylococcus aureus (strain N315)

C:Species: Staphylococcus aureus

C:Date: 10-May-2001 sequence_revision 10-May-2001 *text_change 22-Oct-2001.

C:Accession: E89969

R:Kuroda K. J. Ohta T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cul, L.;

ma, A.; Mizutani-Ul, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kalto, C.; Sekimizu,

C.; Shiba T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.

A:Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus.

A:Accession: E89969

A:Accession: E89969
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J. Bacteriol. J71, 4799-4806, 1989
A:Title: Genetic and molecular analyses of the gene encoding staphylococcal enterotoxin A:Reference number: A33953; MUID:89359112; PMID:25499000
A;Accession: A33953
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A:Gross:references: GB:#28521; NID:gl492109; PIDN:AAB06195.1; PID:g758691
C:Superfamily: enterotoxin B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-258 <BAY>
                                                                                                                                                                                                                                                                      Query Match
Best Local S
                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 25.7%;
Best Local Similarity 35.2%;
Matches 92; Conservative 4
7
               117 IYGVYYKAHCH-GEHQVDTACTYGGVTPHENNKLSEPKNIGVAVYKDNVNVNTFIVTTDK 175
                                 108 IYGVEYYHLCYLCENAERSACIYGGYTNHEGNHLEIPKKIVVKYSIDGIQSLSPDIETNK 167
                                                                                                    59
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             231 YKDNETLDSNTSQIEVYLTTK 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          119 INCYGGE-IDRTACTYGGVTPHEGNKLKERKKIPINLWINGVQKEVSLDKVQTDXKNVTV 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            115 HLCYLCENAERSACIYGGYTNHEGNHLEIPKKIYYKYSIDGIQ-SLSFD-IETNKKMYTA 172
                                                                                                                                                                                                 1 MENNKKYLKKMYFFYLYTFLGLTISQEYFA-QQDPDPSQLHRSSLYK--NLQNIYFLYEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 58 DPVTHENVKSVDQLRSHDLIYN---VSGPNYDKLKTELKNQEMATLFKDKNVDIYGVEYY 114
                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MKKFNILIALLFFTSLVISPLNVKANENIDSVKEKELHKKSELSSTALNNMKHSY--ADK 58
                                                                             NFT - TYKSIVSTTEKFLDFDLLFKSINWLDGISAEFKDLKVEFSSSAISKEFLGKTVD 116
                                                                                                                         DPVTHENVKSV----DQLRSHDLIYN----VSG--PNYDKLKTELKNQEMATLFKDKNVD 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8
                                                                                                                                                             MKNSKVMLN--VLLLILNLIAICSVNNAYANEEDPKIESLCKKSSVDPIALHNINDDYIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YSDNKTLSTEHLHIDIYLYEK 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QELDAQARRYLQKDLKLYNNDTLGGKIQRGKIEFDSSDGSKVSYDLFDVKGDFPEKQLRI 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QELDYKVRKYLTDNKQLYTNGP--SKYETGYIKFIPKNKESFWFDFFPEPEFTQSKYLMI 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LKKM-VFFVLVTFLGLTISQ-EVFAQQDPD---PSQLHR----SSLVKNLQNIYFLYEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NPIIGENKSTGDQFLENTLLYKKFFTDLINFEDLLINFNSKEMAQHFKSKNVDVYPIRYS 118
                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                 25.6%;
                                                                                                                                                                                                                                       ; Score 338; DB 2; Length 260;
; Pred. No. 5.6e-18;
42; Mismatches 107; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 340; DB 2; Length 258;
Pred. No. 4e-18;
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                                                                               C; Superfamily: enterotoxin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C; Genetics:
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A; Residues: 1-136 < KUR>
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A89969
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A:Status: preliminary
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          1 Similarity
91; Conserv
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          Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         49.68;
25.4%; Score 336; DB 2; 34.1%; Pred. No. 7.9e-18; tive 52; Mismatches 86;
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A; Status, France, A; Status, France, Status, France, Status, France, Status, France, Gerba, Gerba, France, Gerba, Gerba, France, Gerba, Gerba, France, Gerba, Marchal Source, Strain N315
                                                                                                                                                                                                                        enterotoxin P [imported] - Staphylococcus aureus (strain N315)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        enterotoxin YENT2 [imported] - Staphylococcus aureus (strain N315)

C:Spate: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001

C:Accession. 89969 #sequence_revision 10-May-2001 #text_change 22-Oct-2001

R:Kurcda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.;

Ma, A.; Milling, T.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu,

Lance, Biba, T.; Battori, M.; Osasavara, N.; Hayashi, H.; Hiramatsu, K.

A:Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus.

A:Reference number: A89788; MUID:21311992; PMID:11418146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A:Cross-references: GB:BA000018; PID:g13701619; PIDN:BAB42912.1; GSPDB:GN00149
A:Experimental source: strain N315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          179 VRKYLTDNKQLYTNGPSKYETGYIKFIPKNKESFWFDFFPE--PEFTQSKYLMIYKDNET 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               125 RSACIYGGVTNHEGNHL-----EIPKKIVVKVSIDGIQSLSFDIETNKKMVTAQELDYK 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               62 VRNYLLKHKNLYEFNSSPYETGYIKFIEGSGHSFWYDLMPESGKKFYPTKYLLIYNDNKT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 KKTCMYGGVTEHDGNQIDKNNSTDNSHNILIKYYENERNSLSFDIPTNKKNITAQEIDYK 61
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Pred. No. 2.9e-18;
Length 260
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A./Folestidnes: 1-288 < KURS-
A.)Cross-references: GB.BA00018; PID:g13701618; PIDN:BAB42911.1; GSPDB:GN00149
A.)Experimental source: strain N315
C;Genetics:
C;Genetics:
C;Genetics: Sen
C;Superfamily: enterotoxin B
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R. Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, I.;

Maa, A.; Misurani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kalto, C.; Sekimizu,

C.; Shiba, T.; Hattori, W.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.

Lancet 357, 1225-1240, 2001 cng of meticillin-resishi, H.; Hiramatsu, K.

A;Tiltis: Whole genome sequencing of meticillin-resishi Stapylococcus aureus.

A;Reference number: A89758; WITD:21311922; PMID:11418146
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C.Specios: Staphylococcus aureus
C.Pate: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
C.Accession: H89968.
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                                                                                                   233 EFFQFYSDNRTVSSSNYHIDVFL 255
                                                                                                                                                                                                      173 AKVTVQELDTKVRFKLENLYKIYNKDTGNIQKGCIFFHSHNHQDQSFYYDLYNVKGSVGA 232
                                                                                                                                                                                                                                                     168 KMVTAQELDYKVRKYLTDNKQLYTNGPSKYETGYIKFIPKN--KESFWFDFFPEPEFTQS 225
                                                                                                                                                                                                                                                                                                         115 YGLYFGNKCVGLTE--EKTSCLYGGVTIHDGNQLDEEKVIGVNVFKDGVQQEGFVIKTKK 172
                                                                                                                                                                                                                                                                                                                                          109 YGYEYYHLCY-LCENAERSACIYGGYTNHEGNHLEIPKKIYYKYSIDGIQSLSFDIETNK 167
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         172 AQELDYKVRKYLTDNKQLYT----NGPSKYETGYIKFIPKNKESFWFDFFPEPEFTQSKY 227
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                                                                                                                                                  226 KYLMIYKDNETLDSNTSQIEVYL 248
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                                                                                                                                                                                                                                                                                                                                                                                                            58 DITWOLD---ESNKISTDOLLNWTIILKNIDISVLKTSSLKVEFNSSDLANGFKGKNIDI 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   53 -FLYEGDPVTHENVKSVDQLRSHDLI---YNVSGPNYDKLKTELKNQEMATLFKDKNVDI 108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MKNIKKLMR--LFYIAAIIITLLCLINNNYVNAEVDKKDLKKKSDLDSSKLF-NLTSYYT 57
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23.6%; Score 311.5; DB 2; Length 258; 33.8%; Pred. No. 5.2e-16; ative 49; Mismatches 102; Indels 23
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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ALIGNMENTS

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MEDLINE-71007902; bubsed-5470821;

Hanng I. Y. Bergdoll M.S.

"The primary structure of staphylococcal

Cyanogen bronide peptides of reduced and
B, and the complate antino soid sequence.
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01-NOV-1991 (Rel. 20, Last sequence update)
15-UNV-2002 (Rel. 41, Last annotation update)
Enterotoxin type C-3 precursor (SEC3),
ENTC3 OR SAV2009 OR SALE17.
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SEQUENCE FROM N.A. STRAIN-Mu50 / ATCC 700699, and N315. MEDLINE-21311952; PubMed-11418146;
                                                                             Staphylococcus aureus.
Bacteria; Firmicutes; Bacillales;
NCHI_TaxID-158878, 158879, 1280;
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2SEB; 28-JAN-98.
3SEB; 27-MAY-98.
1SEB; 16-JUN-97.
1SE4; 15-OCT-97.
1SBB; 04-MAR-99.
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Hattori M., Ogasawara N., Haysshi H., Hiramatsu K.)
                       Nature 36:188-192(1996).

1- SUBCELLIAR LOCATION: Secreted.

1- DISEASE: STARHYLOCOCCAL ENTEROTOXINS CAUSE THE INTOXICAT STARHYLOCOCCAL FOOD FOLSONING SYMBROME.

1- STARHYLOCOCCAL: BELONS TO THE STARHYLOCOCCAL/STREPTOCCCCAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sequence comparison of all three type
enterotoxins.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hovde C.J., Hackett S.P., Bohach G.A.;
"Nucleotide sequence of the staphylococcal enterotoxin C3 gene:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           aureus
                                                                                                                                                                                                                                                                                                                                  MEDLINE=97064178; PubMed=8906797
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Whole genome sequencing of meticillin-resistant Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .ancet 357:1225-1240(2001).
FAMILY.
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                                                                                                                                                                                                                           beta-chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            staphylococcal
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                                                                                             THE INTOXICATION
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Query Match
Best Local S
Matches 117
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PDB; lJCK; I2:NOV-97.

PDB; lJCK; I2:NOV-97.

InterFro; IPRO01961; Stap/Strep_toxin; 1.

Pfam; PF012876; Stap_Strp_tox_C; 1.

PRINTS; PR00279; BACTERITOXIN; 1.

PRINTS; PS00279; STAPH_STREP_TOXIN_1; 1.

PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.

PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
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SEQUENCE
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EMBL; AP003135; BAB43097.1; -.
EMBL; X51661; CAA35972.1; -.
PIR; S11885; S11885.
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117; Conser
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30671, MW;
41.7%; Score 551.5;
46.1%; Pred. No. 5.9
tive 46; Mismatches
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15 VLVTFLGLTIS-QEVFAQQDPD--PSQLHRSS-LVKNLQNIYFLYEGDPVTHENVKSVDQ

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> > FLAHDLIYNISDXKLKNYDKVKTELLNEDLAKKYKDEVVDVYGSNYYVNCYFSSKDNVGK LRSHDLIYNVSG---PNYDKLKTELKNQEMATLFKDKNVDIYGVEYYHLCYLC--ENAER

130 125 70

VTGGKTCMYGGITKHEGNHFDNGNLQNVLVRVYENKRNTISFEVQTDKKSVTAQELDIKA ----SACIYGGYTNHEGNHLEIP--KKIYVKVSIDGIQSLSFDIETNKKMYTAQELDYKV

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                                                                                 PRINTS, PRO0278; BALINLING, TOXIN_1; 1.
PROSITE; PS00277; STAPH_STREP_TOXIN_2; 1.
PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
STAPH_STREP_TOXIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPARISON OF STRUCTURE OF SEA AND SEC2.
MEDLINE-9734373; PubMed-9181079.
Schad E.M., Papageorgiou A.C., Svensson L.A., Acharya K.R.;
A structural and functional comparison of staphylococcal
enterotoxins A and C2 reveals remarkable similarity and
dissimilarity.", Teveals remarkable similarity and
dissimilarity. 129:270-280(1997).
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01-FEB-1994
15-JUN-2002
         DISULFID
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Swaminathan S., Furey W.F. Jr., Pletcl
Residues defining V beta specificity
enterotoxins.";
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MEDLINE-96027099; PubMed-7582894;
Papageorgiou A.C., Acharya K.R., Shapiro R.,
Brehm R.D., Tranter H.S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ETC2_STAAU
P34071;
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                                                                          3D-structure.
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BJ 1875, 22-DEC-96

BJ 187
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SIMILARITY: BELONGS TO THE STAPHYLOCOCCAL/STREPTOCOCCAL TOXIN
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C-2 precursor (SEC2).
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Best Local
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EMBL; X05815; CAA29260.1;
PIR; A01816; ENSAC1.
PIR; S06356; S06356.
                                          use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                      SEQUENCE OF 28-266.
MEDLINE-89131377; PubMed-6189824;
Schmidt J.J., Spero L.;
Schmidt J.J., Spero L.;
"The complete amno acid sequence of
"The schmidt. Chem. 258:6300-6306(1983).
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01-JAN-1990
15-JUN-2002
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between the Swiss Institute of Bioinformatics and the EMBL outs
the European Bioinformatics Institute. There are no restrictions
                                                                                                                                                       -1- SUBCELULAR LOCATION: Secreted.

- DISEASE: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE INTOXICATION STAPHYLOCOCCAL FOOD POISONING SYNDROME.

-1- SINILARITY: BELONGS TO THE STAPHYLOCOCCAL/STREPTOCOCCAL TOXIN
                                                                                                                                                                                                                                                                                        Bohach G.A., Schliever P.M.;

*Nucleotide sequence of the staphylococcal enterotoxin Cl gene relatedness to other pyrogenic toxins.";
                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE-88038352;
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(Rel. 41, Last annotation of type C-1 precursor (SEC1).
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Pfam: PF01113; Stap_Strp_toxin; 1.

Pfam: PF02876; Stap_Strp_tox; 1.

Pfam: PF02876; Stap_Strp_tox; 1.

PROSITE: PR00277; SHCTELFOXIN.

PROSITE: PS00277; STAPH_STREP_TOXIN.1; 1.

PROSITE: PS00278; STAPH_STREP_TOXIN.2; 1.

Enterotoxin; Toxin; Signal; Superantigen.

SIGNAL 1 27 31
Kuroda H., Ohta T., Uchlyama I., Baba T., Yuzawa H., Kobayashi I.,
Cul L., Oguchi A., Aoki K.-I., Ragal Y., Lian J. Q., Ito T.,
Kanamori M., Mateumaru H., Maruyama A., Murakami H., Hosoyama A.,
Mizutani-Ul Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabusaki J.,
Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba
Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.,
Whole genome sequencing of meticillin-resistant Staphylococcus
                                                                                                                                                                         MEDLINE-98298055, PubWed-962503;
Munson S.H., Tremaine M.T., Betley M.J., Welch R.A.;
"Identification and characterization of staphylococcal enterotoxin
types G and I from Staphylococcus aureus.";
priect. Immun. 66:3337-3386(1998).
                                                                                                                                                                                                                                                                                                                              15-JNN-2002 (Rel. 41. Greated)
15-JNN-2002 (Rel. 41. Last sequence update)
15-JNN-2002 (Rel. 41. Last sencestion update)
Enterotoxin type G presureor (SEG):
ENTG OR SEG OR SAVIB24 OR SAL642.
Staphylococcus aureus (strain M35) / ATCC 700699),
Staphylococcus aureus (strain M315), and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
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085382;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STAAM
                                                                                                                  STRAIN-Mu50 / ATCC 700699, and N31 MEDLINE-21311952; PubMed-11418146;
                                                                                                                                   STRAIN-Mu50
                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                   SEQUENCE FROM N.A., AND PARTIAL SEQUENCE STRAIN-FRI572:
                                                                                                                                                                                                                                                                                            Bacteria; Firmicutes; Bacillales; Staphylococcus
NCBI_TaxID=158878, 158879, 1280;
                                                                                                                                                                                                                                                                                                                        Staphylococcus aureus.
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Best Local
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LANCEL 35:1225-1240(2001).
LANCEL 35:1225-1240(2001).
-I SUBCELLULAR LOCATION: Secreted.
-I DISEASE: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE INTOXICATION
-STAPHYLOCOCCAL FOOD POISONING SYNDROME.
-I SIMILARITY: BELONGS TO THE STAPHYLOCOCCAL/STREPTOCOCCAL TOXIN
                                                                                                                                                                                                                                                                                                                                     ETXD_STAAU
P20723;
01-FEB-1991
01-FEB-1991
15-JUN-2002
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIGNAL
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SIGNAL 1 25
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                                                    SEQUENCE FROM N.A. MEDLINE-89359112; PubMed-2549000;
                                                                                                                                                                                                    Staphylococcus aureus 
Bacteria; Firmicutes;
                                                                                                                                                                                                                                                                                                        Enterotoxin
Bayles K.W.,
"Genetic and
                                                                                                                                                                  CBI_TaxID=1280;
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PF02876; Stap_Strp_tox_C; 1.
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Iandolo J.
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41, Last annotation
precursor (SED).
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Pred. No. 1
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BY SIMILARITY.
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RESULT 8
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Matches 92
                             ETXE_STAAU
P12993;
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Pfam; PF02176; Stap_Strp_tox.C; 1.
PRINTS; PR01279; BACTRITOXIN.
PROSITE: PS01277; STAPH_STREP_TOXIN.2; 1.
PROSITE: PS01279; STAPH_STREP_TOXIN.2; 1.
Enterotoxin; Toxin; Signal; Superantigen;
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pIR; A33953; A33953,
HSSP; P13163; 18XT,
InterPro; IPR001961; Stap/Strep_toxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the Swiss Institute of the European Bloinformatics Institute are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for one momercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseeisb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
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-1- SUBCELLULAR LOCATION. SOC:eted.
-1- DISEASE: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE INTOXICATION STAPHYLOCOCCAL FOR DOISONING SYNDROME.
-1- SIMILARITY: BELONGS TO THE STAPHYLOCOCCAL/STREPTOCOCCAL TOXIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The crystal structure of staphylococcal enterotoxin type D reveals 202+-mediated behandlang-tartion."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    enterotoxin
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                                                                                                                                                                                                                                          231
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                                                                                                                                                                                                                                                                                                                                                                                                                                HLCYLCENAERSACIYGGVTNHEGNHLEIPKKIVVKVSIDGIQ-SLGFD-IETNKKMVTA 172
                                                                                                                                                                                      YSDNKTLSTEHLHIDIYLYEK 258
                                                                                                                                                                                                                                          YKONETLOSNTSQIEVYLTTK
                                                                                                                                                                                                                                                                                       QELDAQARRYLQKDLKLYNNDTLGGKIQRGKIEFDSSDGSKVSYDLFDVKGDFPEKQLRI
                                                                                                                                                                                                                                                                                                                                                                                           INCYGGE-IDRTACTYGGYTPHEGNKLKERKKIPINLWINGVQKEVSLDKVQTDKKNVTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NPIIGENKSTGDQFLENTLLYKKFFTDLINFEDLLINFNSKEMAQHFKSKNVDVYPIRYS 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DPVTHENVKSVDQLRSHDLIYN---VSGPNYDKLKTELKNQEMATLFKDKNVDIYGVEYY 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MKKFNILIALLFFTSLVISPLNVKANENIDSVKEKELHKKSELSSTALNNMKHSY--ADK 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LKKM-VFFVLVTFLGLTISQ-EVFAQQDPD---PSQLHR-----SSLVKNLQNIYFLYEG 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    114
258 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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                                                       STANDARD;
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ZINC.
ZINC.
ZINC.
ZINC.
P -> A (IN STRAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 340;
Pred. No. 5.
                                                    PRT;
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                                                                                                                                                                                                                                          251
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4F7C6A28D42597FD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches 102;
                                                       257
                                                    3
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60

AIT-ENKESDDQFLENTLLFKGFFTGHPWYNDLLVDLGSKDATNKYKGKKVDLYGAYYGY PVTHENVKSVDQLRSHDLIYN---VSGPNYDKLKTELKNQEMATLFKDKNVDIYGVEYYH Ş

10 N

KMVFFVLVTELGLTI------SQEVFAQQDPDPSQLHRSSLVKNLQNIYFLYEGD KKTAFILLLFIALTLTTSPLVNGSEKSEEINEKDLRKKSELQRNAL-SNLRQIYY-YNEK

Query Match Matches

Local

66; Similarity

Conservative

49:

98;

Indels

30; Gaps

23.3%;

Score 308; DB 1; Pred. No. 1.6e-16; Mismatches

Length 257; CRC64; METAL CHAIN

METAL SIGNAL

D-structure.

Metal-binding;

SEQUENCE

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27 257 211 249 251 29358 1

ENTEROTOXIN TYPE E.
ZINC (BY SIMILARITY).
ZINC (BY SIMILARITY).
ZINC (BY SIMILARITY).
ZINC (BY SIMILARITY).
CHY: 27EDA94B97770CE3 CRC

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119 QC-AGGTPNKTACMYGGVTLHDNNRLTEEKKVPINLWIDGKQTTVPIDKVKTSKKEVTVQ 116 LCYLCENAERSACIYGGYTNHEGNHLEIPKKIVVKVSIDGIQ-SLSFD-IETNKKMYTAQ

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                                                                                                                   PMBL; M21319; AAA26617.1; -
PIR; A28179; A28179;
PDB; 18EE; 11-OCT-95;
PDB; 18EE; 11-OCT-95;
PDB; 18EE; 11-OCT-95;
PEam; PP01213; Stap_Strp_Loxin; 1.
Pfam; PP012173; Stap_Strp_Lox,C; 1.
Pfam; PP012175; Stap_Strp_Lox,C; 1.
PRINTS; P000279; ASTRH_STRED_TOXIN_1; 1.
PROSITE; P500278; STAPH_STRED_TOXIN_2; 1.
Enterotoxin; Toxin; Signal; Superantigen; Hei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BBBL outstation - the European Bioinformatics Institute on There are no less rigidion on its use by non-profit institutions as long as its content including the modified and this statement is not removed. Usage by mod for form or way entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseeisb-sib.ch)
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01-JAN-1990
15-JUN-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Swaminathan S., Furey W.F. Jr., Pletch Residues defining V beta specificity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3D-STRUCTURE MODELING.
MEDLINE-96022987; PubMed-7552730;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.,
STRAIN-MJB265;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Struct. Biol. 2:680-686(1995).

COPACTOR: Biolds 1 zinc ion per subunit. The zinc ion is necess for the toxin interaction with MHC class II (By similarity).

SUBCELULIAN LOCATION: SOCIENCE SOCIENCE THE INTOXICATION STAPHILOCOCCAL ENTEROTOXINS CAUSE THE INTOXICATION STAPHILOCOCCAL FOOD POISONING SYNDROME.

SIMILARITY: BELONGS TO THE STAPHILOCOCCAL/STREPTOCOCCAL TOXIN
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(Rel. 13, Last sequence update)
(Rel. 41, Last annotation update)
type E precursor (SEE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  170:2954-2960(1988).
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in staphylococcal
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PERSOLTY 9

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AC 9131615
PO 101-JANN
DY 011-JANN
DY 011-
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MEDLINE-6722293; PubMed-3584106;
Huang I.-Y. Hughes J.L., Bergdoll M.S., Schantz E.J.;
"Complete amino acid sequence of staphylococcal enterotoxin J. Biol. Chem. 262:7006-7013(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JAN-1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Enterotoxin type A precursor ENTA OR MW1889.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Staphylococcus aureus (strain MW2), Staphylococcus aureus.
                                                                                                         Swaminathan S., Furey W.F. Jr., Pletch
Residues defining V beta specificity
                                                                                                                                                                                                    The Co-crystal structure of staphylococcal enterotoxin type A with 27-A resolution. Implications for major histocompatibility complex class II binding ;
J. Biol. Chem. 271:32212-32216(1996).
                                                                                                                                                                                                                                                                               Sundstroem M., Hallen D., Abrahmsen L.;
                                                                                                                                                                                                                                                                                                                   X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS). MEDLINE-97113025; PubMed-8943278;
                                                                                                                                                                                                                                                                                                                                                                                                                             Schad E.M., Zaitseva I., Zaitsev V.N., Dohlsten M., Schlievert P.M., Ohlendorf D.H., Svensson L.A.;
                    MEDLINE-97334373; PubMed-9191070;
                                      COMPARISON OF STRUCTURE OF SEA AND SEC2
                                                                          Nat. Struct. Biol. 2:680-686(1995).
                                                                                             enterotoxins.
                                                                                                                                              3D-STRUCTURE MODELING.
MEDLINE-96022987; PubMed-7552730;
                                                                                                                                                                                                                                                                                                                                                                       type A.";
EMBO J. 14:3292-3301(1995).
                                                                                                                                                                                                                                                                                                                                                                                                           *Crystal structure of the superantigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-95354648; PubMed-7628431;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      x-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Betley M.J., Mekalanos J.J.; ^*Nucleotide sequence of the type A staphylococcal enterotoxin gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-88086892; PubMed-3335483;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          acquired MRSA."
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"Genome and virulence determinants
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-22040717;
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  Papageorgiou A.C.,
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                                                                                                                                                                                                                                                                                                 Svensson A.,
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  Svensson L.A.,
                                                                                                                              Pletcher
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                                                                                                            J., Sax M.;
staphylococcal
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  Acharya K.R.;
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                                                                                                                                                                                                                         QC-AGGTPNKTACMYGGVTLHDNNRLTEEKKVPINLMLDGKQNTVPLETVKTNKKNVTVQ
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RDNKTINSENMHIDIYLYT 256 KDNETLDSNTSQIEVYLTT 250 ELDYKVRKYLTDNKQLYTNG--PSKYETGYIKFIPKNKESFWFDFFPEPEFTQSKYLMIY

ELDLQARRYLQEKYNLYNSDVFDGKVQRGLIVFHTSTEPSVNYDLFGAQGQYSNTLLRIY

237

LCYLCENAERSACIYGGVTNHEGNHLEIPKKIVVKVSIDGIQSL--SFDIETNKKMVTAQ

173 118

177

KKTAFTLLLFIALTLTTSPLVNGSEKSEEINEKDLRKKSELQGTAL-GNLKQIY--YYNE

58

Conservative

49:

Mismatches

108;

Gaps

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*A structural and functional comparison of staphylococcal enterotoxins A and C2 reveals remarkable similarity and U. Mailarity. *3. 29:277-280(1997).

1- COPACTOR Binds 1 zinc ion per subunit. The zinc ion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SHISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                          pDB; 185F; 11-JUL-96.
pDB; 185A; 15-OCT-95.
pDB; 185T; 19-NOV-97.
interPro; 1PB001961; Stap/Strep_toxin; 1.
pfam; pP001123; Stap_Strp_toxin; 1.
pkinf5; P00279; BACTRIOXIN.
pkinf5; P00279; BACTRIOXIN.
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                                                                                                                                                                                                                                                                                                  PROSITE; PS00277; STAPH_STREP_TOXIN_1; PROSITE; PS00278; STAPH_STREP_TOXIN_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                Enterotoxin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            for the toxin interaction with SUBUNIT: MONOMER. SUBCELLULAR LOCATION: Secreted.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DISEASE: STAPHYLOCOCCAL EMEROTOXINS CAUSE THE INTOXICATION STAPHYLOCOCCAL FOOD POISONING SYNDROME.
MISCRILANROUS: THIS TOXIN SEEMS TO BE CODED BY A BACTERIOPHAGE SIMILARITY: BELONGS TO THE STAPHYLOCOCCAL/STREPTOCOCCAL TOXIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A28664; A28664.
A29566; A29566.
                  Similarity
                                                                              1
25
120
211
249
251
242
257
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257
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242
                                                                                                                                                                                                                                                                                Signal;
                                                                                    29669 MW;
                  23.28;
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REP_TOXIN_2; 1.
Superantigen;
                                                                                                          ZINC
ZINC
ZINC
                     Pred.
                                       Score 307;
                                                                                                                                                                                                                    ENTEROTOXIN
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ADEBF5BCA1F14677 CRC64;
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                     ĕ.
                  1.8e-16
                                       DB 1; Length 257;
                                                                                                                                                                                                                    TYPE
                                                                                                                                                                                                                                                                                   Metal-binding; Zinc;
Indels
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22;
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EMBL: M91514; AAA27017, 11, ALT_SEQ.
EMBL: M9115; AAA52092, 11, -
EMBL: AB050523; AAA53092, 11, -
EMBL: AB050523; AA35094, 12, -
EMB.; AB0509, A3509,
PDB: 1AN8; 98-APR 98.
InterPro: IPRO15011, Stap/Stipp_tox1
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RRVILINE-92363541; PubMed-1500157;
MEDIJINE-92363541; PubMed-1500157;
MEDIJINE-92363541; PubMed-1500157;
Medison K., Schliavert P. M., Selander R. K., Musser J. M.;
Molecular population genetic evidence of horizontal spread of two
alleles of the pyrogenic exotoxil C gene (spec) among pathogenic
clones of Streptococcus pyogenes.";
Infect. Immun. 60:3313-3317(1992).
                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMPG outstation the European Bioinformatics institute. There are no restrictions on its possible of the content is not restriction on its profit institutions as long as its content is no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseeisb-sib.ch).
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01-JAN-1990
16-OCT-2001
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"Crystal structure of the streptococcal superantigen SPE-C: dimerization and zinc binding suggest a novel mode of interactions of the streptocal superanties of the streptocal supera
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MEDLINE-2119568; PubMed-11295696;
Ferretti J.J., McShan W.M., Ajdic D.J., Savic (
Langhian Y., Jia H.G., Najar F.Z., Ren Q., Zhu H., Song L., Wh.
Yuan Y., Olifton S.W., Roe B.A., McLaughlin R.;
"Complete genome sequence of an Ml strain of Streptococcus
pyogenes."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     with MEC class II molecules.
Nat. Struct. Blol. 4:635-643(1997).
-1- SUBUNIT: Blnds to major histocompatibility complex class II beta
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STRAIN-T18P / MGAS. 1585;
MEDLINE-8831403; PubMed-3045005;
Gomborn S.C., Schllevert P.M.;
*Nucleotide asquence of streptococcal pyrogenic exotoxin
Infect. Immun, 56:2518-2520(1988).
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16-OCT-2001 (Rel.
16-OCT-2001 (Rel.
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Chain: THE STREPTOCOCCAL PYROGENIC TOXINS A. B. AND C ARE DISEASE: THE CAUSATIVE ACENTS OF THE SYMPTOMS ASSOCIATED WITH SCARLET FEVER, HAVE BEEN ASSOCIATED WITH STREPTOCOCCAL TOXIC SHOCK-LIKE DISEASE AND MAY PLAY A ROLE IN THE EARLY EYENTS OF RHEUMATIC
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16-OCT-2001
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                                                                                                                    Perretti J.J., McShan W.M., Ajdic D.J., Savic D.J., Savic G., Primeaux C., Secate S., Suvorov A.N., Kenton S., Lai H.S., Li Primeaux C., Secate S., Suvorov A.N., Kenton S., Lai H.S., White Olan Y., Jia H.G., Najar F.Z., Ren O., Zhu H., Song L., White Yuan X., Clifton S., Roe B.A., McLaujohlin R., "Complete genome sequence of an A. Hattain old Streptococcus pyc Proc. Natl. Acad. Sci. U.S.A. 98.4658-4663 (2001) Proc. Natl. Acad. Sci. U.S.A. 98.458-4663 (2001) Complex class I chain.
                                                                                                                                                                                                                                                                                                              STRAIN-SF370 / ATCC 700294 / Serotype M1; MEDLINE-21192684; PubMed-11296296;
                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                        Streptococcus pyogenes.";
J. Exp. Med. 189:89-102(1999).
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Proft T., Moffatt S.L., Berkahn C.J.,
"Identification and characterization of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-M15;
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                          SUBCELLULAR LOCATION: Secreted.

DISEASE: Mitogenic for human peripheral blood lymphocytes
SIMILARITY: BELONGS TO THE STAPHYLOCOCCAL/STREPTOCOCCAL TY
FAMILY.
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entry is copyright. It is produced through a collaboration is institute of Bioinformatics and the EMBL outstation

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Q9X5C7;
    STRAINSF370 / ATCC 700294 / Serotype MJ MEDLINE-21192684; PubMed-11296296; Ferretti J.J., McShan W.M., Ajdic D.J., Primeaux C., Sezate S., Suvorov A.N., Kk
                                                                                                                                                                                                                                                                                                                 MEDLINE-99093428; PubMed-9874566; Proft T., Moffatt S.L., Berkahn C.
                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                       streptococcus
                                                                                                                                                                                                                                                                                    Proft T., Moffatt S.L., Berkahn C.J.
"Identification and characterization"
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Exotoxin type G precursor
SPEG OR SPY0212.
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Pfem; PF0112; Stap_Strp_toxin; 1.
Pfem; PF0216; Stap_Strp_tox_C; 1.
PR0SITE: PS00277; STAPH_STREP_TOXIN_1;
PROSITE: PS00278; STAPH_STREP_TOXIN_2;
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the European Bioinformatics Institute. These
use by non-profit institutions as long a
modified and this statement is not removed.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VDQLRSHDLIYNVSGPNYDKLKTELKNQEMATLFKDKNVDIYGVEYYHLCYLCENAERSA
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236 AA;
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                                                                                                                                                                                                           pyogenes.";
189:89-102(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           249
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40, Last sequence 40, Last anno
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Pred. No. 2.4e-09;
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A.N., Kenton
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -VNVWDKSKQQPPMFITVNKPKVTAQEVDIKVRKLLIK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Streptococcaceae;
                                 Savic D.J.,
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Lai H.S., Lin
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                                                                                                                          Query Match
Best Local
                                                                Matches
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                                                                                                                                                                              PROSITE; PS00277; STAPH_STREP_TOXIN_1; PROSITE; PS00278; STAPH_STREP_TOXIN_2;
                                                                                                                                                                                                              Pfam; PF01123; Stap_Strp_toxin; Pfam; PF02876; Stap_Strp_tox_C; PRINTS; PR00279; BACTRLTOXIN
                                                                                                                                                                                                                                                                                                                        entitles requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to licensetisb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                         use by non-profit institutions as long a modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                            the
                                                                                                                                                                                                                                                                                                                                                                                                     between the Swiss Institute of Bioinformatics and the EMBL
                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                          SEQUENCE
                                                                                                                                                       SIGNAL
                                                                                                                                                                                                                                                       InterPro; IPR001961; Stap/Strep_toxin
                                                                                                                                                                                                                                                                        HSSP; P13380; 1ANB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       +
                                                                                                                                                                                                                                                                                                                                                                          European Bioinformatics Institute. There are no restrictions by non-profit institutions as long as its content is in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DISEASE: Mitogenic for human peripheral blood lymphocytes. SIMILARITY: BELONGS TO THE STAPHYLOCOCCAL/STREPTOCOCCAL TOXIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                         FAMILY
                                                                                                                                                                                                                                                                                    AF124499; AAD30988.1; -. AE006489; AAK33303.1; -.
                             63 ENVKSVDQLRSHDLIYNVSGPNYDK-----LKTELKNQEMA-----
                                                                                                                                                                  Signal;
                                                                55;
                                                                             Similarity
ENLK--DLKRSLRFAYNITPCDYENVEIAFVTTNSIHINTKQKRSECILYVDSIVSLGIT
                                                                                                                      234 AA;
                                                              Conservative
                                                                                                                                       1
25
                                                                                                                                                                Complete proteome.
                                                                                                                      27262 MW;
                                                                          12.5%;
                                                              40;
                                                          Score 165; DB 1;
Pred. No. 9.3e-06;
0; Mismatches 81;
                                                                                                                                     EXOTOXIN
                                                                                                                                                   POTENTIAL.
                                                                                                                    XOTOXIN TYPE G.
49525C49E4BA2052 CRC64;
                                                                                                                                                                                               FALSE_NEG
                                                                                       Length 234;
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P06886;
01-JAN-1988
01-JAN-1988
15-JUN-2002
 syndrome
J. Biol.
                                                                                                                                                                                                                                                    STAAU
                                          Blomster-Hautamaa D.A.,
Schlievert P.M.;
                                                                   SEQUENCE FROM N.A.,
MEDLINE-87057222; F
                                                                                                                      Staphylococcus aureus.
Bacteria; Firmicutes; Bacillales;
                                                                                                                                                                    Toxic shock
                           "The nucleotide and partial amino acid
                                                                                                              NCBI_TaxID-1280;
                                                                                                                                                                                                                                        TSST_
                                                                                                                                                                                                                                      STAAU
 toxin-1
Chem. 2
                                                                                                                                                             (Rel. 06, Created)
(Rel. 06, Last sequence update)
(Rel. 41, Last annotation updat;
syndrome toxin-1 precursor (TSS'
261:15783-15786(1986)
                                                                                                                                                                                                                                      STANDARD;
                                                                   PubMed=3782090
                                                      Kreiswirth B.N.,
                                                                                                                                                                                                                                     PRT;
                                                                                 SEQUENCE
                                                                                                                      Staphylococcus
                                                                                                                                                                                                                                     234
                                                                                                                                                                 update)
r (TSST-1).
                           sequence of
                                                      Kornblum
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                                                    J.S.,
                           toxic shock
                                                    Novick R.P.,
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214 194

FDFFPEPE - - FTQSKYLMIYKDNETLDS - NTSQIEVYLTT VDLFNKDDKLLSRDSFFKRYKDNKIFNSEEISHFDIYLKT

KETYLPSEAVRIKKKQFTLQEFDFKIRKFLMEKYNIY-DSESRYTSGSLFLATKDSKHYE IQSL--SFDIETNKKMVTAQELDYKVRKYLTDNKQLYTNGPSKYETGYIKFIPKNKESFW

193

134

155

135

84 99

DQFIKGDKVDVFGLPYNFSPPYVDN-----IYGGIVKHSNQGNK---SLQFVGILNQDG

-TLFKDKNVDIYGVEYYHLCYLCENAERSACIYGGVTNH--EGNHLEIPKKIVVKVSIDG

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Presed G.S., Radhakrishnan R., Mitchell D.T., Earhart C.A.
Dingse M.M., Cook W.J., Schlivert P.M., Oblendorf D.H.;
"Refined structures of thee crystal forms of toxic shock
rokin 1 and of a tetramutent with reduced activity.";
protein Sci. 6;1220-123(199).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Acharya K.R., Passalacqua E.F., Jo
Brehm R.D., Tranter H.S.;
"Structural basis of superantigen
structure of toxic-shock syndrome
                                                                                                                                                                                                                                                                                                                                                                                                       Biochemistry 37:7194-7202(1998).
-I- SUBCELLULAR LOCATION: Secreted.
-I- DISEASE: THIS TOXIN IS RESPONSIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                          Earhart C.A., Mitchell D.T., Murray D.L., Pinheiro D.M., Mat
Schllevert P.M., Oblendorf D.H.;
Structures of five mutnants of toxic shock syndrome toxin-1
reduced biological activity.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Structure of toxic shock syndrome Biochemistry 32:13761-13766(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ohlendorf D.H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-94150598;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).
MEDLINE-94150598; PubMed-8107781;
Pfam: PF01123; Stap_Strp_toxin; 1.
Pfam: PF02876; Stap_Strp_tox.C: 1.
PRINTS; PR01501; TOXICSSTOXIN.
PROSITE; PS00277; STAPH_STREP_TOXIN_1;
PROSITE; PS00278; STAPH_STREP_TOXIN_2;
                                                                                                                                         PDB PDB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             X-RAY CRYSTALLOGRAPHY (1.95 ANGSTROMS) OF MEDLINE-98254504; PubMed-9585531;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=97337442; PubMed=9194182;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Papgeorgiou A.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-96319751;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-94092653; PubMed-8268150;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nature 367:94-97(1994).
                                                                  InterPro;
InterPro;
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                                                                                                                                                                                                                                                                                                                                              This
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "The refined crystal structure of toxic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          K-RAY CRYSTALLOGRAPHY (2.07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              K-RAY CRYSTALLOGRAPHY (2.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .07-A resolution
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Structure of toxic shock
                                                                                                                                                                                                                                                                                           European Bioinformatics Institute. The by non-profit institutions as long ified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                      FAMILY.
                                                                                                                                         5TSS;
1QIL;
2QIL;
1AW7;
                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY: BELONGS
                                                                                                                                                                                                                                                                                                                                                                                               SHOCK SYNDROME
                                                                                                                                                                                                                                                                                                                              SWISS-PROT entry is copyright. It is produ
een the Swiss Institute of Bioinformatics
                                                                                                                                                                                            4TSS;
                                                                                                                                                                                                        3TSS;
                                                                                                                                                                                                                                A24606;
                                                                                                                                                                                                                                            J02615;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Biol. 260:553-569(1996).
                                                                                                                                                                                                                                                                                 requires a license agreement
                                                                IPR001961; Stap/Strep_toxin
IPR003999; Staph_toxin.
                                                                                                                                           24 - DEC - 97 .
12 - AUG - 97 .
12 - AUG - 97 .
18 - NOV - 98 .
                                                                                                                                                                                                                                                                     email to license@isb-sib.ch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Earhart C.A.,
                                                                                                                                                                                                                                XCSAS1
                                                                                                                                                                                                                                            AAA26682.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Brehm
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ₽.D.,
                                                                                                                                                                                                                                                                                                                                                                                 TO THE STAPHYLOCOCCAL/STREPTOCOCCAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ANGSTROMS).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ANGSTROMS).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  action inferred
toxin-1.*;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               toxin
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     FALSE_NEG.
                                                                                                                                                                                                                                                                                                                                                                                                           FOR
                                                                                                                                                                                                                                                                                                        There are no restrictions ong as its content is in
                                                                                                                                                                                                                                                                                                                                            is produced through
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                                                                                                                                                                                                                                                                                                                                                                                                           THE SYMPTOMS
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                                                                                                                                                                                                                                                                                           Usage
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R.P.,
                                                                                                                                                                                                                                                                                                                                and the
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                                                                                                                                                                                                                                                                                                                                   EMBL outstation
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Best Local
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                                                                                                                                                                                                                                                                                                            Toxin;
                                           160
                                                                   166
                                                                                        114
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218 K 218
                      226 K 226
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                                                                                                                                                                                                                                                                                                            Superantigen;
                                                                                                                                                                                                                                          Similarity
                                             DKKQLAISTLDFEIRHQLTQIHGLYRS--SDKTGGYWKITMNDGSTYQSDLSKKFEYNTE
                                                                                                                                     SSGSDTFTNSEVLDNSLGSMRIKNTDGSISLIIFPSPYYSPAFTKGEKVDLNTKRTKKSQ
                                                                                                                                                           EGDPVTHENVKSVDQLRSHDLIYNVSG------PNYDKLKTELKNQEMATLFKDKNV
                                                                                                                                                                                                       NKKYLKKWYFFYLYTFLGLTISQEYFAQQDPDPSQLHRSSLYK-----NLQNIYFLY
                                                                   NKKMYTAQELDYKYRKYLTDNKQLYTNGPSKYETGY1KF1PKNKESFWFDFFPEPEFTQS
                                                                                          HTSECTYIHF - - -
                                                                                                              DIYGVEYYHLCYLCENAERSACIYGGVTNHEGNHLEIPKKIVVKVSIDGIQS-LSFDIET
                                                                                                                                                                                  NKKLL--MNFFIVSPLLLATTA-----TDFTPVPLSSNQIIKTAKASTNDNIKDLLDWY
                                                                                                                                                                                                                                                                            234 AA;
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                                                                                                                                                                                                                                                                          26306 MW;
                                                                                                                                                                                                                                          8.2%;
23.2%;
                                                                                                                                                                                                                                                                                                  Signal; 3D-structure
                                                                                                                                                                                                                               35;
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Pred. No. 0.16;
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E95789FF9A1D7AB4 CRC64;
                                                                                          -QISGVTNTE--KLPTPIELPLKVKVHGKDSPLKYGPKF
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USO1_YEAST
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01-MAY 1992 (Rel. 22, Last
16-OCT-2001 (Rel. 40, Last
Intracellular protein tras
USO1 OR INTI OR YDL058W.
                                                                                                                                                     Bal Y., Symington L.S.;
Submitted (MAY-1996) to the EMBL/GenBank/DDBJ
-1- FUNCTION: REQUIRED FOR PROTEIN TRANSPORT E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Saccharomyces cerwisiae (Baker's yeast).
Bukaryola: Rungi, Ascomycota; Saccharomycotina: Saccharomycetes;
Rancharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Saccharomycetales;
NCBI_TaxID=4932;
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                                                                                                                                                                                                                                                                                                   Hostetter M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Nakajima
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-X2180-1A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              USO1_YEAST
P25386;
                                                                                                                                                                                                                    SEQUENCE OF 1-8 FROM
                                                                                                                                                                                                                                                          Submitted (FEB-1993)
                                                                                                                                                                                                                                                                                Kendrick K.E.
                                                                                                                                                                                                                                                                                                                                                                                               "A cytoskeleton-related gene, uso1,
                                                                                                                                                                                                                                                                                                                                                                                                                   Yamasaki M.;
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MEMBRANDS, PROBABLY PRESENT ON VESICLES OPERATIONAL MEMBRANDS, PROBABLY PRESENT ON VESICLES OPERATIONAL REPORT OF AN HEPTAPEPTIDE REPEAT PATTERN CHARACTERISTIC OF AN HEPTAPEPTIDE REPEAT PATTERN CHARACTERS IN THE COILED COILS, MAY EONE HILMENTOUS STRUCTURES IN THE SIMILARITY: BELONGS TO THE VDP/USO1/YBL047C FAMILY.
                                                                                               SUBCELLULAR LOCATION: CYTOPLASMIC. ASSOCIATED WITH INTRACELLULAR MEMBRANES. PROBABLY PRESENT ON VESICLES OPERATIONAL BETWEEN THE
                                                                                                                                        COMPLEX.
                                                                                                                                                                                                                                                                                                                                                            Biol.
                                                                                                                                                                                                                                                                                                                                                         transport in Saccharomyces
Biol. 113:245-260(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                   H., Hirata A.,
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22, Last sequence update)
40, Last annotation update)
tein transport protein USO1.
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RESULTATION OF THE PROPERTY OF
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Best Local S
Matches 62
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Q08554;
Q1-NOV-1997
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16-OCT-2001
                   SEQUENCE FROM N.A.
TISSUE-Foreskin;
MEDLINE-93283349; PubMed-8507556;
Theis D.G., Koch P.J., Franke W.W.;
                                                                                                                                             Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                           Desmocollin
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                                                                                                                                                                                    Homo sapiens (Human)
  'Differential synthesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            European Bioinformatics Institute.
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L03188; AAB00143.1; -.
U53668; AAB66659.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   62; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              s requires a license agreement (S)
an email to license@isb-sib.ch).
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(Rel.
1A/1B
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40,
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precursor (Desmosomal glycoprotein 2/3) (DG2/DG3).
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                                                                                                                                             Primates;
                                                                                                                                                              Chordata;
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  of type 1 and type 2 desmocollin mRNAs
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COILED COIL (POTEWTIAL);
CHANGED (DIT (POTEWTIAL);
DISPENSABLE FOR THE PROTEIN FUNCTION.
ASP(GLU MICH (ACIDIC);
5 > 8 (IN REF. 2);
7 > 1 (IN REF. 2);
7 > 1 (IN REF. 2);
8 > 8 (IN REF. 2);
9 > 1 (IN REF. 2);
1 > 9 (IN REF. 2);
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Pred. No. 3.
                                                                                                                                           Craniata; Vertebrata;
Catarrhini; Hominidae
                                                                                                                                                                                                                                                                                                                             PRT;
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EMBL; Z34522; CAA84278.1; -.
EMBL; X72925; CAA51428.1; -.
EMBL; X72925; CAA51429.1; -.
HSSP; P15116; 1NcJ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the END person Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/mnnounce/
                                                                                                                                                                                                                                                                                                                                             Pfam; PF00028; cadherin; PRINTS; PR00205; CADHERIN SMART; SM00112; CA; 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE-Foreskin;
                                                                                                                                                                                                                                                                                   Cell adhesion;
                                                                                                                                                                                                                                                                                                      PROSITE; PS50268; CADHERIN_2; 5
                                                                                                                                                                                                                                                                                                                                                                                                                           MIM; 125643;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Genew; HGNC:3035;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                related to the desmosomal cadherins DGII/III."; FEBS Lett. 286:9-12(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       King I.A., Magee A.I., Rees D.A., Buxton R.S.; "Keratinization is associated with the expression of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 135-151 AND 283-292.
MEDLINE-91323543; PubMed-1713860;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-94116981; PubMed-8288219;
King I.A., Arnemann J., Spurr N.K.,
"Cloning of the cDNA (DSC1) coding
its assignment to chromosome 18.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (JUN-1994)
                                                                                                                                                                 TRANSMEN
                                                                                                                                                                                                                                               SIGNAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genomics 18:185-194(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             rissue-skin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR002126; Cadherin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE SPECIFICITY: STRONGLY EXPRESSED IN EPIDERMIS, LESS NODE AND TONGUE.

DOMAIN: CALCIUM MAY BE BOUND BY THE CADHERIN-LIKE REPEATS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DDHESTYBNESS BETWEEN CELLS THAT EXPRESS DIFFERENT ISOFORMS. LINKED TO THE KENATINIZATION OF EPITHELIAL TISSUES.
SUBCELLULAR LOCATION: Type I membrane protein.
ALTERNATIVE PRODUCTS: 2 ISOFORMS; 1A/DG2 (SHOMN HERE) AND 1B/DG3;
ARE PRODUCTS UP ALTERNATIVE SELUCING.
TISSUE SPECIFICITY: STRONGLY EXPRESSED IN EPIDERMIS, LESS IN LYMPH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (POTENTIAL).
SIMILARITY: CONTAINS 5 CADHERIN DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IN THE INTERACTION OF PLAQUE PROFEINS AND INTERNEDIATE FILAMENTS
MEDIATING CELL-CELL ADDRESION. MAY CONTRIBUTE TO PEIDERNAL CELL
POSITIONING (STRATIFICATION) BY MEDIATING DIFFERENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FUNCTION: COMPONENT OF INTERCELLULAR DESMOSOME JUNCTIONS. INVOLVED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      stratified epithelia.";
J. Dev. Biol. 37:101-110(1993).
                                                                                                                                                                                                                                                               ; Glycoprotein; Transmembrane;
Calcium-binding; Alternative :
                                                                                                                                                                                                                                                                                                                                                                    CADHERIN.
                                                                                                                                                                                                                                                                                                                             CADHERIN_1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 DSC1
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                                                                             POTENTIAL.
CYTOPLASMIC (POTENTIAL).
CADHERIN 1.
CADHERIN 2.
CADHERIN 3.
CADHERIN
CADHERIN
N-LINKED
N-LINKED
                                                                                                                                                                               DESMOCOLLIN 1A/1B.
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                            ; Alternative POTENTIAL.
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RSPLIC		840	KVYLCGODEEH -> ESIRGHTLIKN (IN ISOFORM	
			18).	
RSPLIC	841	894	MISSING (IN ISOFORM 1B).	
NFLICT	132	132	T -> S (IN REF. 3).	
QUENCE	894 AA;	100044	W; 44BA33038699E3E1 CRC64;	
Match Local S	imilarity	7.9%; 19.8%;	Score 105; DB 1; Length 894; Pred. No. 1.7; 4: Mismarches 78: Indels 84: Gara	5.
34	PDPSQLHRS	SLVKNLQNI	FLYEGDPVTHENVKSVDQLRSHDLIYNVSGPNYDKLKTELK	93
138	PIPASLMEN	SLGPFPQHV-	QQIQS-DAAQNYTIFYSISGPGVDKEPFNLF	185
94	NOEMAT L	FKDKNVDIYO	VEYYHLCYLCENAERSACIYGGVTNHEGNHLEIPKKIVVKV	151
186	YIEKDTGDI	FCTRSIDRE	YEQFALYGYATTADGYAPEYPLPLIKI	232
152	SIDGIQSLS	PDIE	YKVRKYLTDNKQ	188
233	EDDNDNAPYI	FEHRVTIFTY	PENCRSGTSVGKVTATDLDEPDTLHTRLKYKILQQIPDHPK	292
189	LYTNGPSKYI	ETGYI	FIPKNKESEWFDPF	217
293	HFSIHPI	TGVITTTTE	FLDREKCDTYQLIMEVRDMGGQPFGLFNTGTITISLEDEND	349
	PEPEFTQSK	218 PEPEFTQSKYLMIYKDN 234	34	
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Result
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Δ	<u>,,,</u>			PS00277;	PR00279; BACTRLTOXIN.	PF02876; Sta	PF01123; Sta	InterPro; IPR001961;	P08095; 1B1Z.		X61559; CAA4					٠.	Med. 174:1		ding pyro	"Characterization and clonal distribution of four	Nelson K., Schlievert P.M., Selander R.K.,	MEDLINE-92044323; PubMed-1940804;	STRAIN-MGAS156, AND	SEQUENCE FROM N.A.		[D-1314;	Streptococcaceae; Streptococcus.	Bacteria; Firmicutes;	Streptococcus pyogenes		exotoxin precursor			997 (TrEMBLrel	P97164;	PRELIMINARY;	
22	_		STAPH_STREP_TOXIN_2;	STAPH_STREP_TOXIN_1;	ACTRLTOXI	Stap_Strp_tox_C;	Stap_Strp_toxin;	1; Stap/Strep_	· ·	3752.1; -	CAA43757.1; -	CAA43756.1; -	3753.1; -	CAA43758.1; -	CAA43755.1; -	CAA43754.1; -	174:1271-1274(1991).	pyogenes.";	pyrogenic exotoxin A (scarlet	and clona	ert P.M.,	PubMed-19	D MGAS500;				Streptoco	es; Bacil	enes.				•	Lrel. 03,		INARY;	
POTENTIAL			EP_TOXIN_	EP TOXIN	Z	(C:	xin; 1.	trep_toxin.		•	•	•	•	•	•	•	1991).		toxin A (l distrib	Selander	40804 :	••				ccus.	Bacillus/Clostridium group;			(Fragment).		Last seq	Created)		PRT;	
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR001961; Stap/Strep_toxin. Pf01123; Stap_Strp_toxin; 1. Pfam; PF03876; Stap_Strp_tox.C; 1. Pfam; PF03876; Stap_Strp_tox.C; 1. PRINTS; PR00279; BACTRLTOXIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Streptococcus pyogenes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nelson K., Schlievert P.M., Selander R.K., M. "Characterization and clonal distribution of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-MGAS624 AND MGAS158 AND MGAS485 AND MGAS491,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Streptococcaceae;
NCBI_TaxID-1314;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Firmicutes; Bacillus/Clostridium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Type A exotoxin precursor (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-92044323; PubMed-1940804;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EQUENCE FROM N.A.
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35; Conservative
                                                                                                                                                                         Similarity
                        PS00277;
PS00278;
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STAPH_STREP_TOXIN_2;
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                                                                                                                                Score 1239; DB 2;
Pred. No. 4.7e-81;
"""matches 1;
                                                                                                                                                                                                                                                                                                                  TYPE A EXOTOXIN.
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Pred. No. 4
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                                                                                                                                                                                                                                                             29DF2AD575623A84 CRC64;
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of four alleles of the t fever toxin) in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           group; Lactobacillales;
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                                                                                                                                                                                                                 Query Match
Best Local Sin
Matches 234;
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Nelson K. Schllevert P.M. Selander R.K., Mussi

*Characterization and closel distribution of fo

gene encoding pyrogenic exotoxin A (scarlet few

Strept-coccus pyrogens.;

J. Exp. Med. 174:1271-1274(1991).

EMBL: 861562; CCA43760.1;

EMBL: 861562; CCA43761.1;

EMBL: 861567; CCA43762.1;

EMBL: 861567; CCA43762.1;

EMBL: 861567; CCA43762.1;

EMBL: 861567; CCA43762.1;

EMBL: 861566; CCA43763.1;

EMBL: 861566; CCA43762.1;

EMBL: 861566; CCA43762.1;

EMBL: 861566; CCA43762.1;

EMBL: 861566; CCA43763.1;

EMBL: 8615666; CCA43763.1;

EMBL: 8615666; CCA43763.
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SEQUENCE
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Q57453;
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Bacteria; Firmicutes; B
Streptococcaceae; Strep
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01-NOV-1996 (TrEMBLrel.
01-MAR-2002 (TrEMBLrel.
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Pfam; PF01123; Stap_Strp_toxin; I.
Pfam; PF02876; Stap_Strp_tox; C; 1.
Prints; PR00279; BACTRLTOXIN.
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                                                                    KKMVFFVLVTFLGLTISQEVFAQQDPDPSQLHRSSLVKNLQNIYFLYEGDPVTHENVKSV
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milarity 99.2%;
Conservative
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27484 MW;
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STAPH_STREP_TOXIN_2;
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Last annotation update)
                                                                                                                                                                                                                 Score 1234; D
Pred. No. 1.1e
0; Mismatches
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of four
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Best Local Similarity
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Bacteria; Firmicutes; Bacillus/Clostridium
Streptococcaceae; Streptococcus.
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01-MAY-2000 (TrEMBLrel.
01-MAR-2002 (TrEMBLrel.
                                                                                                                        Q54696;
Q54696;
Q1-NOV-1996
Q1-NOV-1996
Q1-MAR-2002
Type A exot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bessen D.E. Tzzo M.W., Fiorentino T.R., Bullingshead S.K., Beall B.; Genetic linkage of exotoxin alleles and tropism group A streptococci ". Infect. Plan 179:627-36(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Exotoxin A (Fragment).
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                                               SPEA.
Streptococcus pyogenes.
Bacteria; Firmicutes; Bacillus/Clostridium
Streptococcaceae;
NCBI_TaxID=1314;
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222 AA;
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                                                                                                                                                                                                                                                               PRELIMINARY;
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                             Streptococcus
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Pred. No. 2.2e
0; Mismatches
                                                                                                                                   (Fragment)
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                                                          group; Lactobacillales;
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Streptococcaceae; NCBI_TaxID=1314;

MEDLINE-99137798; PubMed-9952369;

emm Caringal

gene

markers R.M.

for

STRAIN-D633 SEQUENCE FROM N.A. Streptococcus pyogenes Bacteria; Firmicutes; Bacillus/Clostridium

group;

Lactobacillales;

Streptococcus.

Exotoxin SPEA

type A (Fragment).

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무. 왕
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Best Local S
Matches 209
Q9S5Z4 PRELIMINARY;
Q9S5Z4;
01-MAY-2000 (TrEMBLrel. 1
01-MAY-2000 (TrEMBLrel. 1
01-MAR-2002 (TrEMBLrel. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nelson K., Schlievert P.M., Selander R.K., Musser J.M.;
"Characterization and clonal distribution of four alleles
gene encoding pyrogenic exotoxin A (scarlet fever toxin)
Streptococcus pyrogenies.",
J. Exp. Med. 174-12171-1214 (1991).
BMDL; X61573; CAA43771-1;
HSSP: p80695; 1812.
                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR001961; Stap/Strep_toxin.
Pfam, Pf0112; Stap_Strp_toxin; 1.
Pfam, Pf01213; Stap_Strp_tox.C: 1.
Pfam; Pf02876; Stap_Strp_tox.C: 1.
PRINTS; PR00277; STAP; STREP_TOXIN_1.
PR051TE; PS00277; STAP; STREP_TOXIN_1.
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NON_TER
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NON_TER
SIGNAL
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SEQUENCE FROM N.A.
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                                                                                                                                              IYGGVTNHEGNHLEIPKKIYVKVSIDGIQSLSFDIETNKKMVTAQELDYKVRKYLTDNKO 188
                                                                                                                                                                                                                                                                                                                            236 AA;
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22
23
236
27575 MW;
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STAPH_STREP_TOXIN_2;
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 Created)
Last sequence update)
Last annotation update)
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Pred. No. 8.
                                                                                                                                                                                                                                                                                                                                                TYPE A EXOTOXIN.
                                               PRT;
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alleles of the spear
toxin) in
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RESULT POPULATION OF THE POPUL
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Persence of streptococcal pyrogenic exotoxin A and C gene isolates of group G Streptococci.*;

Sublates of group G Streptococci.*;

R BELL ANGSTA: ANGOGGE,1.*

R PERS. ANGSTA: PRODUST: Streptoxin: 1.

R PERS. PROSIDE: PERST. PLOXIN: 1.

R PERS. PROSIDE: PROSI
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Best Local :
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Best Local S
Matches 198
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01-DEC-2001 (TremBLrel.
01-DEC-2001 (TremBLrel.
01-MAR-2002 (TremBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Streptococcus equisimilis.

Bacterla; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
Streptococcaecae; Streptococcus.

NCBL_TaxID-119602;
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PROSITE;
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NON_TER
SEQUENCE
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Similarity 89.2%; Pred. No. 7e-68;
98; Conservative 12; Mismatches ;
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LEIPKNILVKYSIDGIQSLSFDIETSKKMYTAQELDYKVRKHLTDNNQLYTNGPSKYETG
                           LEIPKKIVVKYSIDGIQSLSFDIETNKKMYTAQELDYKVRKYLTDNKQLYTNGDSKYETG
                                                                                                            SGLNYDKLKTELKNREMSTLFKNKNVDIYGVEYYYHCYLCRNAKRRACIYGGVTNHEGNH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LEIPKNILVKYSIDGIQSLSFDIETSKKMYTAQELDYKVRKHLTDNNQLYTNGPSKYETG
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PS00278;
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222 AA;
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222 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                          222
25884 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STAPH_STREP_TOXIN_1; 1.
STAPH_STREP_TOXIN_2; 1.
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25884 MW;
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89.2%;
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20,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Created)
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Pred. No. 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                   121F8460992818F8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121f8460992818f8 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                            DB 2; Length
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RESULT
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Q9 AC Q9 AC
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Best Local Similarity
Matches 115; Conserv
                                                                                                                  Q53678; PRELIMINARY;
Q53678;
01-NQV-1996 (TrEMBLrel. 0
01-NOV-1996 (TrEMBLrel. 0
01-MAR-2002 (TrEMBLrel. 2
                                            Staphylococcus aureus. Bacteria; Firmicutes;
                                                                                            Enterotoxin (Fragment).
NCBI_TaxID=1280;
                         Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIATES-2056668; PubMed-11114901;
Fitzgarald J.R., Monday S.R., Foster T.J., Bohach G.A., Hartigan Meaney H.J., Smyth C.J., Schuck T.J., Bohach G.A., Hartigan Characterization of a putative pathogenicity island from bovine Staphylococcus aureus encoding multiple superantigens.*;
Bacceriol. 18:63-70(2001).
MBL, AF21733; AAC29599.1;
INTERTPOLYSIS, AAC29599.1;
INTERTPOLYSIS, AAC29599.1;
FRAMTS, FRO1023; Stap_Strp_toxin.
FRAMTS, FRO123; Stap_Strp_toxin.
FRAMTS, FRO0279; BACTRITOXIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
SEQUENCE 271 AA; 31267 MW; 3493F6228B042F10 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16; Last seq
01-UN-2002 (TrEMBLrel. 21, Last anno
Staphylococcal enterotoxin C-bovine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q9FOL6;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  178 KVRKYLIDNKOLYINGPSKYETGYIKFIPKNKESFWFDFFPEP--EFTQSKYLMIYKDNE
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                                                                                                                                                                                                                                                                                                                                                                                       TLDSNTSQIEVYLTTK 251
                                                                                                                                                                                                                                                                                                                                                                 TVDSKSVKIEVHLTTK 269
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DKFLAHDLIYNISDKKLKNYDKVKTELLNEDLAKKYKDEVVDVYGSNYYVNCYFSSKDNV
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                                 Bacillus/Clostridium group; Bacillales;
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                                                                                                                  Last sequence update)
Last annotation update)
                                                                                                                                                                             Created)
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Pred. No. 3
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Best Local S
Matches 111
                                   PROGUTE: PS00278; STAPL_STREP_TOXIN.1: 1.

PEBM: P10375; AAA26619.1; .

HSSP: P34071: ISE2.

INTERFEO: IPR001961; STAP/STREP_TOXIN.1: PEBM: PF02876; STAP_STREP_TOXIN.1: 1.

PEBM: PF02876; STAPL_STREP_TOXIN.1: 1.

PROSITE: PS00279; STAPL_STREP_TOXIN.1: 1.

PROSITE: PS00278; STAPL_STREP_TOXIN.1: 1.
                                                                                                                                                                                                                                                                Q06532;
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01-NOV-1996 (TERMBLTE1. 01. Last sequence update)
01-MAR-2002 (TERMBLTE1. 20. Last annotation update)
Enterotoxin type C-7 (SEC740N) (Fragment).
Staphylococcus aureus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro. IPR001961; Stap/Strep_toxin.
Pfam; PF021123; Stap_Strp_toxin; 1.
Pfam; PF021123; Stap_Strp_toxin; 1.
Pfam; PF0216; Stap_Strp_tox; 1.
PROSITE; PF00279; BACTRITOXIN,
PROSITE; PF00279; STAPH_STREP_TOXIN_1;
PROSITE; PF00278; STAPH_STREP_TOXIN_2;

TOX. TOXINGER PF00278; TAPH_STREP_TOXIN_2;

TOXINGER PF00278; TAPH_STREP_TOXIN_2;
Enterotoxin; Toxin; NON_TER 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Firmicutes; Bacillus/Clostridium group;
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MAIX J.C., Lyon J.D., Roberson J.R., Lupher M. B
"Characterization of novel type C staphylococcal
biological and evolutionary implications.";
Infect. Immun. 614284 4262 (1993).
EMBL. L13376; AAA26600.1;
TESP. P340712, 1882.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=94011313; PubMed=8406814;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-740N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=1280;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Staphylococcus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ETGYIKFIPKNKESFWFDFFPEP--EFTQSKYLMIYKDNETLDSNTSQIEVYLTTK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   239 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      41.78;
                     Superantigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27618 MW; A13E7EB25C6989C2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 551; DB 2;
Pred. No. 6e-32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
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                                                                                                                                                                                                                                                                       S. PYOGENES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14;
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5 B 5 B

86

140 HLEIP--KKIVVKVSIDGIQSLSFDIETNKKMVTAQELDYKVRKYLTDNKQLYTNGPSKY

121 197

DKVKTELLNEDLAKKYKDEVVDVYGSNYYVNCYFSSKDNVGKVTGGKTCMYGGITKHEGN

DKLKTELKNOEMATLFKDKNVDIYGVEYYHLCYLC--ENAER----SACIYGGVTNHEGN 139

SQPDPTPDELHKSSEFTGTMGNMKYLYDDHYVSATKVKSVDKFLAHDLIYNISDKKLKNY

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                                                                             Query Match
Best Local Similarity
Matches 110; Conserv
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                                                                                                                                                                                                                                                              BMGL: L1378; AAA6622.1;

BSSP: P34071 JSTE; Stap/Strep_toxin.

Ffam; P70173; Stap_Strp_toxin; 1.

Ffam; P70276; Stap_Strp_tox; 1.

FRANTS; PR00279; BACTRITOXIN.

PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1

PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local
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Q06533;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-94011313; PubMed-8406814;
MART J.C., Lyon J.D., Roberson J.R., Lupher M., Bohach G.A.;
"Characterization of novel type C staphylococcal enterotoxins:
biological and evolutionary implications.";
Infect. Immun. 61:4254-4264(193).

-1- DISEASE: STAPHYLOCOCCAL ENTEROTOXINS ANUSE THE INTOXICATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1996 (TREMBLREL, 01, Created)
01-NOV-1996 (TREMBLREL, 01, Last sequence update)
01-MAR-2002 (TREMBLREL, 20, Last annotation update)
Enterotoxin type C (SECCOPELAND) (Fragment).
Staphylococcus aureus.
                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                       NON_TER
                                                                                                                                                                                                                                               Enterotoxin; Toxin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STAPHYLOCOCCAL FOOD POISONING SYNDBOME.

1- SIMILARITY: THE DIFFERENT S. NIBEUS ENTEROTOXINS AND S. PYOGENES
PYROGENIC EXOTOXINS ARE ALL RELATED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. STRAIN-MNCOPELAND;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID-1280;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales, Staphylococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       182
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AQQDPDPSQLHRSS-LVKNLQNIYFLYEGDPVTHENVKSVDQLRSHDLIYNVSG---PNY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AQQDPDPSQLHRSS-LVKNLQNIYFLYEGDPVTHENVKSVDQLRSHDLIYNVSG---PNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ETGY I KFIENNGNTFWYDMMPAPGDKFDQSKYLMMYNDNKTVDSKSVKIEVHLTTK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DKYKTELLNEDLAKKYKDEVYDYYGSNYYYNCYFSSKDNYGKYTGGKTCMYGGITKHEGN 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DKLKTELKNQEMATLFKDKNVDIYGVEYYHLCYLC--ENAER----SACIYGGVTNHEGN
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                                                                                                                                                                                         239 AA; 27651 NW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   239
                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
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                                                                                                                                                                                                                                           Superantigen.
                                                                             41.5%; Score 549; D)
46.6%; Pred. No. 8.40
tive 45; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   44;
                                                                                                                                                                                         A21A954386AE8625 CRC64;
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                                                                                                                               В
                                                                                                        .4e-32;
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                                                                                                                               Length 239;
                                                                             Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   237
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Bohach G.A.;

enterotoxins:

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A SAN SOCIO
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Best Local S
Matches 112
                                                                                        Enterotoxin type C-4 (SEC4446) (Fragment). Staphylococcus aureus. Bacteria; Findicutes; Bactlius/~1...
Staphylococcus aureus.
                                                                                                                                                                                                  Q06531;
01-NOV-1996 (TrEMBLrel.
01-NOV-1996 (TrEMBLrel.
01-MAR-2002 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam: PP01133; Stap_Strp_Loxin; 1.
Pfam: PP0216; Stap_Strp_Lox, C: 1.
PRINTS: PR00279; BACTRIFOXIC: 1.
PROSITE: PR00278; STAPH_STREP_TOXIN_2;
PROSITE: PS00278; STAPH_STREP_TOXIN_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Edwards V.M., Deringer J.R., Callantine S.D., Deobald C.I.
Berger P.H., Kapur V. Stauffcher C.V., Behach G.A.;
'Characterization of the type C enterotoxia (SEC canine)
Staphylococcus Intermedius pyoderms isolates.',
Summittee (FEB-197) to the EMBL/GenBank/DDBJ databases.
BMBL: U91536; AMS50248.1;
ISSP: P23131, 10CK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JUL-1997 (TrembLrel. 04, 01-JUL-1997 (TrembLrel. 04, 01-MAR-2002 (TrembLrel. 20,
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                              SEQUENCE FROM N.A
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42; Mismatches
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Best Local S
Matches 111
                           MAIT J.C., JANO J.D., Roberson J.R., Lupher M., Bohach of "Characterization of novel type C staphylococcal enterot biological and evolutionary implications.";

Infect. Immun. 61.4284-4282(1993).

-1 DISABLES: SYNPHYLOCOCCAL ENTEROTOXINS CAUSE THE INTOX STAPHYLOCOCCAL FOOD POISONING SYNDROME.

-1 SHILLRATTY: THE DIFFERENT S. AUREUS ENTEROTOXINS AND PROCENIC EXOTOXINS ARE ALL RELATED.

-1 SHILLRATTY: AURICA STAPPLICATION.

REMED: 13377; AAAC632.1; -

REMED: 13377; AAAC632.1; -

REMED: 12377; AAAC632.1; 
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Q06535
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HSSP: P34071; ISB2.
Interpro; IPRO01961; Stap/Strep_toxin.
Pfam: PF01123; Stap_Strp_toxin; 1.
Pfam: pF02076; Stap_Strp_tox.C; 1.
PRINTS; PR00279; BACTRLTOXIN.
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-1- SIMILARITY: THE DIFFERENT S. AUREUS ENTEROTOXINS AND S. PYOGENES
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"Characterization of novel type C staphylococcal
biological and evolutionary implications";
Infect. Immun. 61:4254-4262(1993)
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Best Local :
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                                                                                                                                                                                                          HSSP, P4071, 1522

HSSP, P4071, 1522

InterPro; IPR001961; Stap/Strep_toxin.

Pfam; PF01123; Stap_Strp_toxin; 1.

Pfam; PF02173; Stap_Strp_toxin; 1.

Pfam; PF0275; Stap_Strp_toxic; 1.

PRINTS; PR00279; BACTRLITOXIN.

PROSITE; PS00279; STAPH_STREP_TOXIN_1; 1.

PROSITE; PS00279; STAPH_STREP_TOXIN_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                     **Marr J.C., Lyon J.D., Roberson J.R., Lupher M., Bohach G.A.;

**Characterization of novel type (s taphylococcal enterotoxins:
blological and evolutionary implications.*;

Infect. Immun. 61.4254-4262(199).

-1- DISASSE: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE INTOXICATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1996 (TERMBLrel. 01, Created)
01-NOV-1996 (TERMBLrel. 01, Last sequence update)
01-MAR-2002 (TERMBLrel. 20, Last annotation update)
Enterotoxin type C (SECOVINE) (Fragment).
                                                                                                                                                                                                                                                                                                                                      STAPHYLOCOCCAL FOOD POISONING SYNDROME.

--- SHMILMRITY: THE DIFFERENT S. AREBUS ENTEROTOXINS AND S. PYOGENES
PYROGENIC EXOTOXINS ARE ALL RELATED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE-94011313; PubMed-8406814;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Enterotoxin; Toxin; NON_TER 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE: PS00277; STAPH_STREP_TOXIN_1; 1. PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                 Enterotoxin; Toxin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID-1280;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
Staphylococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Staphylococcus aureus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                182 ETGYIKFIESNGNTFWYDMAPAPGDKFDQSKYLMIYKDNKMYDSKSVKIEVHLTTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   122
                                                                                                      109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             140 HLEIP--KKIVVKVSIDGIQSLSFDIETNKKMVTAQELDYKVRKYLTDNKQLYTNGPSKY 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              109;
                                                                       30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 62
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  86 DKLKTELKNOEMATLFKDKNVDIYGVEYYHLCYLCENAERS-----ACIYGGVTNHE 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         86 DKLKTELKNQEMATLFKDKNVDIYGVEYYHLCYLCEN-----AERSACIYGGVTNHEGN 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ν
                                                                                                                     Similarity
                                     SQPDPTPDELHKASKFTGLMENMKVLYDDRYVSATKVKSVDKFLAHDLIYNISDKKLKNY
                                                                    AQQDPDPSQLHRSSLVKNL-QNIYFLYEGDPVTHENVKSVDQLRSHDLIYNVSG---PNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ETGYIKFIPKNKESFWFDFFPEP--EFTQSKYLMIYKDNETLDSNTSQIEVYLTTK 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HFDNGNLQNVLIRVYENKRNTISFEVQTDKKSVTAQELDIKARNFLINKKNLYEFNSSPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DKYKTELLNEDLAKNYKDEYYDYYGSNYYVNCYFSSKDNYGKYTSGKTCMYGGITKHEGN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SQPDPMPDDLHKSSEFTGTMGNMKYLYDDHYVSATKVKSVDKFLAHDLIYNINHKKLNNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AQQDPDPSQLHRSS-LVKNLQNIYFLYEGDPVTHENVKSVDQLRSHDLIYNVSGP---NY
                                                                                                                                                                  239 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            239 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative 43; Mismatches
                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27648 MW; CC3CB3B04E4119E0 CRC64;
                                                                                                                 45.88;
                                                                                                                                                                  27517 MW; F354742619C8D196 CRC64;
                                                                                                                                                                                                 Superantigen.
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46.2%; Pred. No. 1.9e-31;
                                                                                                 : Score 539; DB 2; Length 239; Pred. No. 4.3e-31; 48; Mismatches 63; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    239 AA
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DKVKTELLNEDLAKKYKDEVVDVYGSNYYVNC--CFSSKDNVGKVTGGKTCMYGGITKHE

Search completed: June 23, 2003, 16:14:55 Job time: 40.7024 secs

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Sequence 33, Appl
Sequence 4, Appl
Sequence 80, Appl
Sequence 222, A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-765-272-222
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 27, Application US/10002784A Publication No. US20030036644A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Ulrich, Robert G
-10-002-784A-27
                                                                                                                                                                                                                                                                                                                                                    (without alignments)
2102.722 Million cell updates/sec
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1 MOGDPDPSQLHRSSLVKNLQ......ALGTGGGAGGFNGYQSAVVG 468
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                               GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compug
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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61 TELKNQEMATLEKDKNIDIYGVEYYHLCYLCENAERSACIGGVTNREGNHLEIPKKIVVK 120 121 VSIDGIQSLSFDIETNKKMVTAQELDYKVRKYLTDNKQLYTNGPSKYETGYIKFIPKNKE 180 61 TELKNQEMATLFKDKNIDIYGVEYYHLCYLCENAERSACIGGVTNREGNHLEIPKKIVVK 120 9 9 1 MQQDPDFSQLHRSSLVKNLQNIYFLXEGDPVTHENVKSVDQLRSHDLIYNVSGPNYDKLK 1 MOODPDPSQLHRSSLVKNLQNIYFLYEGDPVTHENVKSVDQLRSHDLIYNVSGPNYDKLK SFWFDFFPEPEFTQSKYLMIYKDNE'LDSNTQIEVYLTTKQPVVKSLLDSKGIHYNQGNP ô Length 468; Indels Ouery Match 100.0%; Score 2500; DB 9; Best Local Similarity 100.0%; Pred. No. 1.2e-185; Best Local Similarity 0. Mismatches 0; Mismatches 0; . OTHER INFORMATION: mutant SpeA-mutant SpeB fusion US-10-002-784A-27 181 셤 å ö

Sequence 16, A Sequence 13, A Sequence 13, Sequence 12, Sequence 12, Sequence 12, Sequence 8, Ap

Sequence 12,

US-09-870-759-12

Sequence Seq

US-10-002-784A-6 US-10-002-784A-10 US-08-882-431-10 US-08-882-431-14 US-10-002-784A-14 US-10-002-784A-8

Sequence 27, Sequence 25,

Sequence

US-10-002-784A-25 US-10-002-784A-24 US-10-002-784A-36 US-08-882-431-16 US-08-882-431-16 US-09-881-784A-16 US-09-870-759-10 US-09-870-759-10

Description

SUMMARIES

В

Query Match Length

Score

Result ĕ

ORGANISM: Artificial sequence

LENGTH: 468

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95 ERSACI-GGVTNREGNHLEIPKKIVVKVSIDGIQSLSPDIETNK-KMVTAQELDYKVRKY 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         213 IEVYLIT---KQPVVKSLLDSKGIHYNQGNPYNLLIPVIEKVKPGEQSFVGQHAATGCVA 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          389 WEAQIDKELSQNQPVYYQG-GKVGGHAFVIDGADGRNFYHVNWGWGGVSDGFFRLDALNP 447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 115 WEAQIDKELSQNQPVYYQGVGKVGGHAFVIDGADGRNFYHVNWGWGGVSDGFFRLDALNP 374
                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: mutant streptococcal pyrogenic exotoxin B prosegement US-10-002-784A-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            --TYAGTAEIKQPVVKSLLDSKGIHYNQGNPYNLLTPVIEKVKPGEQSFVGQHAATGCVA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                153 LTDNKQLYTNGPSKYETGYIKFIPKNKESFWFDFFPEPEFTQSKYLMIYKDNETLDSNTQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 47 OKSAAIKAGARSAEDIKLD---KVNLGGELSGSNMYGYNISTGGFVIVSGDKRSPEILGY
                                                                                                                                                                                                                                                                                                                                                                                                          39;
                                                                                                                                                                                                                                                                                                                                                           53.0%; Score 1324.5; DB 9; Length 398; Similarity 71.1%; Pred. No. 1.16-94; Scoretvative 20; Mismetches 49; Indels 39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 220;
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CURRENT APPLICATION NUMBER: US/10/002,784A
CURRENT FILING DATE: 2001-11-36
PRIOR APPLICATION NUMBER: 08/082,431; 09/144,776
PRIOR FILING DATE: 97-06-25; 98-09-01
TITLE OF INVENTION: Bacterial Superantigen Vaccines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 9;
                  FILE REPRENENCE (00/2/3/2/8/A)
CURRENT APPLICATION WABRER: US, 0002,784A
CURRENT FILIND DATE: 3001-11-56
PRION APPLICATION WABRER: 08/882,431; 09/144,776
FRION FILING DATE: 97.06-23; 98.09-01
NUMBER OF SEG ID NOS: 40
SEG ID NO 24
SEG ID NO 24
LENGTH: 398
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   448 SALGTGGGAGGFNGYQSAVVG 468
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                                                                                                                                                                                                                                                   ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Artificial sequence
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                                                                                                                                                                                                                                                                                                                                                                                                             Matches 273; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 40
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                     341 ADVGISYDADY OPSSCSAGSSRYQRALKENFGYNQSYHQITRESDFSODWEAQIDKELSON 400
121 ADVGISYDADYOPSSGSAGSSRYQRALKENFGYNGSYHQINREDFSQDWEAQIDKELSON 180
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                                                                                                                                                                                                                              9
                                                                                                                NHPKNLFAAISTRQYNWNNILPTYSGRESNVQKMAISELMADVGISVDMDYGPSSGSAGS
                                                                                                                                         221 QPVVKSLLDSKGIHYNGGNPYNLLTPVIEKVKPGEQSFVGQHAATGCVATATAQIMKYHN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            401 QPVYYQGGKVGGHAFVIDGADGRNFYHVNWGWGGVSDGFFRLDALNPSALGTGGGAGGFN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Gaps
                                                                                                                                                                                                                                                                                                                        DGRNFYHVNWGWGGVSDGFFRLDALNPSALGTGGGAGGFNGYQSAVVG 468
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TITLE OF TRYBRING: Backerial Superantigen Vaccines
FILE REPERENCE: 003/333/SAP
CURRENT PAPLICATION WUMBER: 02/10/002,784A
CURRENT FILING DATE: 2001-11-26
PRIOR RAPLICATION NUMBER: 08/082.431; 09/144,776
PRIOR FILING DATE: 97-06-25; 98-09-01
NUMBER OF SEQ ID NOS: 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              53.3%; Score 1332; DB 9;
100.0%; Pred. No. 1.5e-95;
tive 0; Mismatches 0;
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ORGANISM: Artificial sequence
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Matches 248; Conservative
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RESULT 2 US-10-002-784A-25

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                                                                                                         US-08-882-431-16
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                                                      Matches 217;
                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.5
SOFTWARE: Microsoft Word 6.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: Bacteria.
TITLE OF INVENTION: Vaccines
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Mark A. Olson
APPLICANT: Sina Bavari
                                                                                                                                                                                                        TELEFAX: (301) 619-7714
NEORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Microsoft Wo
                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 619-2065
                                                                                                                                                                                                                                                                                                      ATTORNEY / AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                       MOLECULE TYPE: Pept
                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
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CITY: I
                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: U:
FILING DATE: June 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 21702-5012
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE:
                                                                                                                                                                                                                                                                        NAME: Moran, John
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                 TYPE: Amino I
                                                                                                                                                                              LENGTH:
                                                                                                                                                                                                                                 TELEPHONE:
                                                                    Local Similarity
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FORT DETRICK
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                                                                                                                                                                  Amino Acid
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US Army MRMC -504 Scott Street MCMR-JA (John Moran-Patent Atty)
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                                                      Conservative
                                                                                                                           Peptide
                                                                                                                                                       Unknown
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                                                                      45.4%;
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                                                                                                                                                                                                                                                                              26,313
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                                                      Score 1136; DB 1;
pred. No. 2.4e-80;
1; Mismatches 1;
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                                                                                        Length 251;
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US-08-973-391A-13

Sequence 13, Application US/08973391A
Fatent No. USZ0020054887A1
GENERAL INFORMATION:
APPLICANT: Schilevert, Patrick M.
APPLICANT: Schilevert, Manuela
APPLICANT: Moggiant, Manuela

APPLICANT: StockY Jennifer
APPLICANT: Oblendorf, Douglas
TITLE OF INFERTION: MUTANTS OF STREPTOCOCCAL
FILE REFERENCE: 600.3110840
CURRENT APPLICATION MUMBER: US/08/973,391A
CURRENT FILING DATE: 1998-03-12
PRIOR APPLICATION WIMBER: PCT/US98/10252
PRIOR PRIING DATE: 1996-06-07

TOXIN A AND METHODS OF USE

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TITLE OF INVENTION BACTERIAL Superantigen Vaccines
FILE REFERENCE: 003/233/SAP
CURRENT APPLICATION NUMBER: US/10/002/784A
CURRENT FILING DATE: 2001-11-26
PRIOR PETILING DATE: 97-06-25, 98-09-01
NUMBER OF SED ID NOS: 40
SOFTWARE: Apple MacIntosh Microsoft Word 6.0
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; Sequence 16, Application US/10002784A
; Publication No. US20030036644A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Ulrich, Robert G.
                                                                                                                                                                                                                                                                                                                Matches 217;
                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE: OTHER INFORMATION: streptococcal pyrogenic exotoxin-A mutant
                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                                                                      Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 VSIDGIOSLSFDIETNKKMYTAQELDYKVRKYLTDNKQLYTMSDSKVETGYIKFIPKNKE 180
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                                    181 SFWFDFFPEPEFTQSKYLMIYKDNETLDSNT-QIEVYLTTK 220
                                                                                                                                                         91 ELKNQEMATLFKDKNVDIYGVEYYHLCYLCENAERSACIYGGVTNHEGNHLEIPKKIVVK 150
                                                                                                                                                                                                                                  31 QQDFDPSQLHRSSLVKNLQNIYFLYEGDPVTHENVKSVDQLRSHDLIYNVSGPNYDKLKT 90
                                                                                                                                                                                                                                                                      2 QQDPDPSQLHRSSLVKNLQNIYFLYEGDPVTHENVKSVDQLRSHDLIYNVSGPNYDKLKT 61
                                                                                                                                                                                                                                                                                                                                 h 45.4%;
Similarity 98.2%;
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                                                                                                                                                                                           ELKNOEMATLFKDKNIDIYGVEYYHLCYLCENAERSACI-GGVTNREGNHLEIPKKIVK 120
                                                                                                                                                                                                                                                                                                                   Conservative

    Mismatches

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pred. No. 2.4e-80;
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; TYPE: PRT
; ORGANISM: Streptococcus pyogenes
US-09-870-759-20
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                                                                                                                                                                                                                                                                                                 Query Match
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                                                               Post Pocal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 20, Application US/09870759 Patent No. US20020177551A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICAVI: TERMAN, David S
TITLE OF INVENTION: COMPOSITIONS AND METHO
FILE REFERENCE: 870759
CURRENT APPLICATION NUMBER: US/09/870,759
CURRENT FILING DATE: 2002-01-14
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PRIOR FILING DATE: 1995-06-07
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PATENTIN VERSION 3.1
SEQ ID NO 13
                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: US 60/208,128
PRIOR FILING DATE: 2000-05-30
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                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 250
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                                                                                                                     65 NOEMATLFKOKNIDIYGVEYYHLCYLCENAERSACI~GGVTNREGNHLEIPKKIVYKVSI 123
                                                                                                                                                                                                                                                             185; Conservative
                                                                                                                                                                                    34 PKPSQLQRSNLVKTFKIYIFFMRVTLVTHENVKSVDQLLSHDLIYNVSGPNYDKLKTELK 93
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 VSIDGIQSLSFDIETNKKMYTAQELDYKVRKYLTDNKQLYTNGPSKYETGYIKFIPKNKE 180
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                                                                            ``^GIOSLSFDIETNKKMVTAOELDYKVRKYLTDNKOLYTNGDSKYETGYIKFIPKNKESFW 183
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EPEFTQSKYLMIYKDNETLDSNTSQIEVYLTTK 250
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                               PEFTQSKYLMIYKDNETLDSNT-QIEVYLTTK 220
                                                          FDIEQIKN-GNCSR1SYTYRKYLTDNKQLYTNGPSKYETGYIKFIPKNKESFW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
                                                                                                                                                                                                                                                                          37.5%;
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Pred. No. 4.7e-65;
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Pred. No. 2.9e-79;
1; Mismatches 3;
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US-09-870-759-10
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                                                                                Query Match
Best Local (
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SEQ ID NO 10
LENGTH: 266
TYPE: PRT
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LENGTH: 239
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-09-150-947B-12
                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: TERMAN, David S
TITLE OF INVENTION: COMPOSI
FILE REFERENCE: 870759
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 10, Application US/09870759
Patent No. US20020177551A1
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                                                                                                                                                                                                                                                                   CURRENT FILING DATE: 2002-01-14
PRIOR APPLICATION NUMBER: US 60/208,128
PRIOR FILING DATE: 2000-05-30
NUMBER OF SEQ ID NOS: 166
                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/870,759
CURRENT FILING DATE: 2002-01-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 21.7%; Score 543; DB 10: Length 239; Best Local Similarity 48.1%; Pred. No. 2e-34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 114; Conservative
                                                                                                                                                       ORGANISM: Staphylococcus aureus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: BROAD SPECTRUM PYROGENIC TITLE OF INVENTION: ANTACONISTS AND VACCINES FILE REFERENCE: A31957-PQT-08A, a CURRENT APPLICATION NUMBER: US/09/150,947B CURRENT FILING DATE: 1996-09-10 PRIOR APPLICATION NUMBER: PCT/119/700438 PRIOR FILING DATE: 1997-12-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 12, Application US/09150947B Patent No. US20020028211A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: PRIOR FILING DATE: 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Kaempfer, Raymond APPLICANT: Arad, Gila
                                                              113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    183 ETGYIKFI-ENENSFWYDMMPAPGDKFDQSKYLMMYNDNKMVDSKDVKIEVYLTTKK 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          168 ETGYIKFIPKNKESFWFDFFPEP--EFTOSKYLMIYKDNETLDS-NTQIEVYLTTKO 221
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2 QQDPDPSQLHRSSLVKNL-QNTYFLYEGDPVTHENVKSVDQLRSHDLTYNVSGP---NYD 57
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                                                                             Similarity
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                                                        Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1996-12-30
                                                              21.5%; Score 541; DB 9; Length 266; 47.7%; Pred. No. 3.2e-34;
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                                         39; Mismatches
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; ORGANISM: bean
US-10-151-336-8
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    CURRENT APPLICATION NUMBER: US/10/002,784A
CURRENT FILING BATE: 2001.11-26
PRIOR APPLICATION NUMBER: 08/882,431; 09/144,776
PRIOR FILING BATE: 97-06-29; 98-09-01
NUMBER OF SEQ ID NOS: 40
SED THE APPLE MACINIOSH MICROSOft Word 6.0
SED ID NO 6
                                                                                                                                                                                         GENERAL INFORMATION:
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                                                                                                                     APPLICANT: Ulrich, Robert G.
TITLE OF INVENTION: Bacterial Superantigen Vaccines
FILE REFERENCE: 003/233/SAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/10/151,336
CURRENT FILING DATE: 2002-05-20
PRIOR APPLICATION NUMBER: US/09/414,276
PRIOR FILING DATE: 1999-10-07
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TITLE OF INVENTION: Genenit Virus Vectors for Gene Expression in Plants
FILE REFERENCE: 4868/84453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Mason, Hugh
APPLICANT: Palmer, Ke
APPLICANT: Hefferon,
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Mor, Tsafrir
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Pred. No. 4.6e-34;
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SOFTWARE: Apple Macintosh Microsoft Word 6.0
SEQ ID NO 10.
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Best Local
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PRIOR APPLICATION NUMBER: 08/882,431;
PRIOR FILING DATE: 97-06-25; 98-09-01
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TITLE OF INVENTION: Bacterial Superantigen Vaccines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILE REFERENCE: 003/233/SAP
                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Artificial sequence
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                                                                                                                                                                                                                                                                                                                 21.2%; Score 530; DB 9
47.3%; Pred. No. 2e-33;
tive 39; Mismatches
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Pred. No. 1.6e-33
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RESULT 15
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                                   GENERAL INFORMATION
                                                     Sequence 8, Application US/10002784A Publication No. US20030036644A1
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Best Local S
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 239
APPLICANT: Ulrich, Robert G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM;
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.5
SOFTWARE: Microsoft Word 6.0
CURRENT APPLICATION DATA:
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APPLICANT:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 619-2065
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: Unknown MOLECULE TYPE: Pept:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US FILING DATE: June 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: Amino Acid
STRANDEDNESS: Unknown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 21702-5012
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TF: US Army MRMC -504 Scott Street MCMR-JA (John Moran-Patent Atty)
FORT DETRICK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             h 21.0%;
Similarity 46.4%;
                                                                                                                                                                                    ETGYIKFIPKNKESFWFDFFPEP--EFTQSKYLMIYKDNETLDS-NTQIEVYLTTKQ 221
                                                                                                                                                                                                                                                                                                                                                                                     QPDPKPDELHKSSKFTGKMENMKVLYDDNHVSAINVKSIDQFRYFDLIYSIKDTKLGNYD
                                                                                                                                                                                                                                         GNQLDKYRSITVRVFEDGKNLLSFDVQTNKKKYTAQELDYLTRHYLVKDKKLYEFNNSPY 182
                                                                                                                                                                                                                                                                          GNHLEIPKKIVVKVSIDGIQSLSEDIETNKKMVTAQELDYKVRKYLTDNKQLYTNGPSKY 167
                                                                                                                                                                                                                                                                                                                                                                                                                        QQDPDPSQLHRSS-LYKNLQNIYFLYEGDPYTHENYKSYDQLRSHDLIYNYSGP---NYD 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MARYLAND
                                                                                                                                                               ETGYIKFI-ENENSFWYDMMPAPGDKFDQSKYLMMYNDNKMYDSKDVKIEVYLTTKK 238
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Sina Bavari
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 525; DB 1;
Pred. No. 4.8e-33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 239;
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CURRENT APPLICATION NUMBER: US/10/002,784A
CURRENT FILMS DATE: 2001-11-26
FRIOR APPLICATION NUMBER: 05/682,431; 09/144,776
FRIOR FILING DATE: 97-06-25; 98-09-01
NUMBER OF SEO ID NOS: 40
SOFTWARE: APPLE MACINTOSH Microsoft Word 6.0
SEO ID NO 8
SEO ID NO 8
SEO ID NO 8
DENOTH: 266
LENGTH: 266
DEGANISM: Artificial sequence
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US-10-002-784A-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
   210
                                           168
                                                                                      150
                                                                                                                                 108 GNIILEIPKKIVVKVSIDGIQSLSFDIETNKKMYTAQELDYKVRKYLTDNKQLYTNGPSKY 167
                                                                                                                                                                                                                       58
                                                                                                                                                                            90 NVRVEFKNKDLADKYKDKYVDVFGANAYYQCAFSKKTNDINSHQTDKRKTCMYGGVTEHN 149
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                        ETGYIKFIPKNKESFWFDFFPEP--EFTQSKYLMIYKDNETLDS-NTQIEVYLTTKQ 221
ETGYIKFI-ENENSFWYDMMPAPGDKFDQSKYLMMYNDNKMVDSKDVKIEVYLTTKK 265
                                                                                      GNQLDKYRSITVRVFEDGKNLLSFDVQYNKKKVTAQELDYLTRHYLVKNKKLYEFNNSPY 209
                                                                                                                                                                                                                       KLKTELKNQEMATLFKDKNIDIYGVEYYHLCYLCENA-----ERSACI-GGVTNRE 107
                                                                                                                                                                                                                                                                   QPDPKPDELHKSSKFTGLMENMKYLYDDNHVSAINVKSIDQFRYFDLIYSIKDTKLGNYD 89
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46.8%; Pred. No. 1
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7;

Search completed: June 23, 2003, 16:16:39 Job time: 25.0835 secs

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OM protein - protein search, using sw model
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No.
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Maximum DB seq length: 2000000000
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Perfect score:
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Listing first 45 s
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                                                                                                                                       1095.5
1095.5
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Gapop 10.0 , Gapext 0.5
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1 MQQDPDPSQLHRSSLV
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Match
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1: sp_archea:*
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Copyright (c) 1993 - 2003 Compugen Ltd.
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ALIGNMENTS

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054779 PRELHKNARY, PRT: 236 AA. 054779; 054781; 054735; 054736; 054741; 01.40V-1396 (TPEMBLEAL. 01. Greated) 01-40V-1396 (TPEMBLEAL. 01. Last sequence update) 01-40R-2012 (TPEMBLEAL. 20) Last annotation update) Type A exotoxin precursor (Fragment).
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"Role of CsrR, hasA, and spels genes in the internalization Streptococcus pyogenes by epithelial cells.";
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, X035865, AAK71464.1;
MEROPS; C10.001;
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Pfam; PF01640; Peptidase_C10; 1.
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STRAIN-SP268;
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     RESULT OF RESULT
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Best Local S
Matches 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gene encoding pyrogenic exotoxin A (scarlet fe
Streptcoccus pyogenes.*,
J. Exp. Ned. 174 1271-1274(1991).
EMBL; X61569; CAA43770.1.
EMBL; X61572; CAA43770.1.
EMBL; X61569; CAA43766.1.
EMBL; X61570; CAA43768.1.
EMBL; X61571; CAA43768.1.
EMBL; X61571; CAA43768.1.
                                                                                                                                                                                                                           Q9R931;
01-MAY-2000
01-MAY-2000
01-MAR-2002
Exotoxin A ()
     MEDLINE-99137798; PubMed-9952369; Bessen D.E., Izzo M.W., Fiorentir Hollingshead S.K., Beall B.;
                                                                                                                      Streptococcus pyogenes.
Bacteria; Firmicutes; Bacillus/C
Streptococcaceae; Streptococcus.
NCBI_TaxID-1314;
                                                                   STRAIN-D709;
                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                Q9R931
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CHAIN
NON_TER
SEQUENCE
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NON_TER
SIGNAL
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Pfam; PP01123; Stap_Strp_toxin; 1.
Pfam; PP02876; Stap_Strp_toxin; 1.
Pfam; PP02876; Stap_Strp_tox; 1.
Pfam; PP02876; Stap_Strp_tox; 1.
PR0STIE: P800279; BACTRLTOXIN.
PR0STIE: P800278; STAPH_STREP_TOXIN.1;
PROSTIE: P800278; STAPH_STREP_TOXIN.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nelson K., Schlievert P.M., Selander R.K., Musser "Characterization and clonal distribution of four
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-MGAS624 AND MGAS158 AND MG
MEDLINE-92044323; Pubmed-1940804;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Streptococcaceae; Streptococcus.
NCBI_TaxID-1314;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Streptococcus pyogenes, Bacillus/Clostridium group; Lactobacillales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SPEA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       181
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                                                                                                                                                                                                                                                                                                                                                                                                                             SFWFDFFPEPEFTQSKYLMIYKDNETLDSNT
                                                                                                                                                                                                                              A (Fragment).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VSIDGIQSLSFDIETNKKMVTAQELDYKVRKYLTDNKQLYTNGPSKYETGYIKFIPKNKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ELKNQEMATLFKDKNIDIYGVEYYHLCYLCENAERSACIYGGVTNHEGNHLEIPKKIVVK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ELKNQEMATLFKDKNIDIYGVEYYHLCYLCENAERSACI-GGVTNREGNHLEIPKKIVVK
                                                                                                                                                                                                                                               (TrEMBLrel.) (TrEMBLrel.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    236
                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
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23
236
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22
23 >236
3 236
4; 27468 MW; 43.9°
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98.6%;
                                                                                                                                                                Bacillus/Clostridium
     Fiorentino
1 B.;
                                                                                                                                                                                                                                               13,
                                                                                                                                                                                                                                               Created)
Last sequence up
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 1096.5; DB 2;
Pred. No. 3.9e-62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0
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TYPE A EXOTOXIN
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                         T.R.,
                                                                                                                                                                                                                                                                                                                              222
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                         Caringal R.M.
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                                                                                                                                                                                                                                                                update)
                                                                                                                                                                group;
                                                                                                                                                                                                                                               update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Musser J.M.;
of four alleles
fever toxin) i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MGAS491,
                                                                                                                                                                Lactobacillales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length
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202 180 142

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P97 110 P97 11
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Best Local S
Matches 207
                                                                                                                                                                                                                            gene encoding pyrogenic exotoxin A Streptcoccus pyrogenes;

J. Exp. Med. 174:1271-1274(1991).

EMBL: X61555; CAAA3754.1:

EMBL: X61555; CAAA3758.1:

EMBL: X61555; CAAA3758.1:

EMBL: X61558; CAAA3758.1:

EMBL: X61558; CAAA3757.1:

EMBL: X
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P97163; P97164;
01-MAY-1997 (Tre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Genetic linkage of exotoxin alleles and tropism in group A streptococci; Junicer Dis. 179:637-636(1999).
EMBL, AR055699, AND1624.1;
HSSF: P08095; IBLZ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-MGAS156, AND MGAS500;
MEDLINE-92044323; PubMed-1940804;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Streptococcus pyogenes.
Bacteria; Firmicutes; Bacillus/Clostridium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Type A exotoxin precursor SPEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAY-1997 (TREMBLIEL 03, 01-MAY-1997 (TREMBLIEL 03, 01-MAR-2002 (TREMBLIEL 20, 01-MAR-2002 (TREMBLIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IRR001961; Stap/Strep_toxin.
Pfam; PF01123; Stap_Strp_toxin; 1.
Pfam; PF02876; Stap_Strp_tox; 1.
Pfam; PF02876; Stap_Strp_tox; 1.
Pfan; PF02878; Stap_Stry_tox; 1.
PR05178; PF002779; PF02878; STREP_TOXIN_1;
PR05178; P500278; STAPH_STREP_TOXIN_2;
         Signal
                                                                         PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Streptococcaceae; Streptococcus.
NCBI_TaxID=1314;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NON_TER
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                                    Pro: IPR001961; Stap/Strep_toxin.
10 Pr01123; Stap_Strp_toxin; 1.
10 Pr02876; Stap_Strp_tox_C: 1.
178; PR00279; BACTRATOXIN.
178: PS00279; TAPH_STREP_TOXIN_1;
178: PS00278; STAPH_STREP_TOXIN_1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          191
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      131
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QQDPDPSQLHRSSLVKNLQNIYFLYEGDPVTHENVKSVDQLRSHDLIYNVSGPNYDKLKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEWEDEFPEFETQSKYLMIYKDNETLDSNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VSIDGIQSLSFDIETNKKMVTAQELDYKVRKYLTDNKQLYTNGPSKYETGYIKFIPKNKE 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ELKNQEMATLFKDKNVDIYGVEYYHLCYLCENAERSACIYGGVTNHEGNHLEIPKKIVVK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           222
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8
                                STAPH_STREP_TOXIN_1; 1.
STAPH_STREP_TOXIN_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                222
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Created)
Last sequence up
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 1095.5; DB 4;
Pred. No. 4.1e-62;
"" "" anatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ₹
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lactobacillales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ۲,
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PRINTS; PR02979; BACTRITOXIN
PROSITE; PS00277; STAPH_STREP_TOXIN_1;
PROSITE; PS00278; STAPH_STREP_TOXIN_2;
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Characterization and clonal distribution o 
gene encoding pyrogenic exotoxin A (scarlet 
Streptococcus gyrogenes; exotoxin A (scarlet 
g., Exp., Med. 174:1271-274(1991).
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Score 1089.5; DB 2;
Pred. No. 1.1e-61;
1; Mismatches 3;
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Pred. No. 4.5e-62;
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TYPE A EXOTOXIN.
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Characterization and cloud. Iditribution of four at
gene encoding pyrogenic exotoxin A (scarlet fever to:
Streptococcus pyrogenic exotoxin A (scarlet fever to:
J. Exp. ked. 174.1271-1274(1991).
EMBL. M61573, CAM.3771.1;
EMBL. M61573, CAM.3771.1;
INTOFFO: IFRO01561, Stap.Strp.Loxin.
Pfam. PF00173; Stap.Strp.Loxin.
Pfam. PF0172; Stap.Strp.Loxin.
Pf0172; Pf00777; STAPH_STREP_TOXIN.1; 1.
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  SFWFDFFPEPEFTQSKYLMIYKDNETLDSNT
                                                                                                                                                                                                                                      QQDPNPSQLHRSSLVKNLQNIYFLYEGDPVVHENVKSVDQLLSHDLIYNVSGLNYDKLKT
                                                                                                                                                                                                                                                              QQDPDPSQLHRSSLVKNLQNIYFLYEGDPVTHENVKSVDQLRSHDLIYNVSGPNYDKLKT
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                                                              VSIDGIQSLSFDIETSKKMYTAQELDYKVRKHLTDNKQLYTNGPSKYETGYIKFISKDKE
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                                                                                                                                                                                                                                                                                                                          Score 986.5; I
Pred. No. 3.7e
13; Mismatches
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Best Local s
Matches 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tropism in group & streptococci;

J. Infect. bis. 179:637-636(1999).

EMBL; AF029051; AAD21131.1:

InterPro; IPRO10961; Stap/Strep_toxin.

Pfam; PF09123; Stap_Strp_tox(1.

Pfam; PF0916; Stap_Strp_tox(2.1.

PROSTIE; BR00279; STAPH_STREP_TOXIN_1: 1

PROSTIE; PS00278; STAPH_STREP_TOXIN_2: 1

PROSTIE; PS00278; STAPH_STREP_TOXIN_2: 1
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Q9S5Z4;
Q1-MAY-2000
                                                                                                                                                                                                                                   Q938P4;
                                                                             Streptococcus equisimilis.

Bacteria; Firmicutes; Bacillus/Clostridium
                                                                                                                                                              01-DEC-2001 (TrEMBLrel. 19, 01-DEC-2001 (TrEMBLrel. 19, 01-MAR-2002 (TrEMBLrel. 20,
SEQUENCE FROM N.A
                                                              Streptococcaceae;
                                                                                                                             SPEA.
                                                                                                                                               Pyrogenic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Streptococcaceae;
NCBI_TaxID=1314;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAY-2000
01-MAR-2002
                                      NCBI_TaxID-119602;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Streptococcus pyogenes.
Bacteria; Firmicutes; Bacillus/Clostridium
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=99137798; PubMed=9952369;
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222 AA;
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Pred. No. 7.1e
13; Mismatches
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                                                                             group; Lactobacillales;
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Best Local Similarity
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053678
01-NOV-1996 (TrEMBLrel 0
01-NOV-1996 (TrEMBLrel 0
01-NOV-1996 (TrEMBLrel 0
01-MAR-2002 (TrEMBLrel 2
Enterotoxin (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIANS-9011313" PubMed-8406814,
MET JC. Lipon JD. Roberson JR. Lupher M., B
"Characterization of novel type C staphylococcal
'Characterization of novel type C staphylococcal
bloidylcal and evolutionary implications.";
Infect. Immun. 51:4234-4262(1993).
MEDI. Li3376. MAX5650.1;
MEDI. Li3376. MAX5650.1;
MEDI. Li3376. P40(1) 1582.
                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR001961; Stap/Strep_toxin, Pfam; PF01123; Stap_Strp_toxin; 1. Pfam; PF02876; Stap_Strp_tox_C; 1. Pfam; PF02879; BACTRLTOXIN.
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Pfam: PF02876; Stap_Strp_tox_C; 1.
PR0SITE: PS00277; STAPH_STREP_TOXIN_1;
PR0SITE: PS00278; STAPH_STREP_TOXIN_2;
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Submitted (AUG-2011) to the EMBL/GenBank/DDBJ databases.
EMBL, AY046743, AAL06068.1.
InterPro, 178001961; Stap/Strep_toxin.
                                                                                                                                                                                                                                                                                                                                          PROSITE; PS00277; STAPH_STREP_TOXIN_1;
PROSITE; PS00278; STAPH_STREP_TOXIN_2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          185;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        131
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              71
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                                                                                                                                                                            Similarity
QPDPTPDELHKASKFTGLMENMKVLYDDRYVSATKVKSVDKFLAHDLIYNISDKKLKNYD
                                                              QQDPDPSQLHRSSLVKNL-QNIYFLYEGDPVTHENVKSVDQLRSHDLIYNVSG---PNYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VSIDGIQSLSFDIETSKKMVTAQELDYKVRKHLTDNNQLYTNGPSKYETGYIKFISKDKE
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                                                                                                                                                                                                                                                                            239 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            222
222 AA;
                                                                                                                                           Conservative
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25884 MW;
                                                                                                                                                                                                                                                                       27618 MW; A13E7EB25C6989C2 CRC64;
                                                                                                                                                                       20.6%;
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                                                                                                                            Score 516; DB 2; L
Pred. No. 2.7e-25;
"" matches 69;
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Pred. No. 7.1e
13; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     239
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                                                                                                                                                                                                    Length 239;
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RESULT 12
Q06532
ID Q0653
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Best Local :
 Q06532;
Q06532;
Q1-NOV-1996
Q1-NOV-1996
Q1-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PP01123; Stap_Strp_toxin; 1.

Pfam; PP02176; Stap_Strp_tox_C; 1.

PRLNTS; PR00276; Stap_Strp_tox_C; 1.

PROSITE: PS00277; STAPH_STREP_TOXIN_1: 1.

PROSITE: PS00277; STAPH_STREP_TOXIN_2: 1.

SEQUENCE 271 AA; 31267 MM; 3493F6228BI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Staphylococcal enterotoxin C-bovine SEC-BOV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  09F0L6;
01-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q9F0L6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Staphylococcus aureus encoding multiple J. Bacteriol. 183:63-70(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fitzgerald J.R., Monday S.R., Foster T.J., Meaney W.J., Smyth C.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAR-2001 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AF217235; AAG29599.1;
HSSP; P34071; 1SE2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE=20566668;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Staphylococcus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Staphylococcus aureus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR001961; Stap/Strep_toxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Characterization of a putative pathogenicity island
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID-1280;
                                                                                                                                                    169
                                                                                                                                                                                 155
                                                                                                                                                                                                    111 LEIPK--KIVVKVSIDGIQSLSFDIETNKKMYTAQELDYKVRKYLTDNKQLYTNGPSKYE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 183
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           111 LEIPK--KIVVKVSIDGIQSLSFDIETNKKMVTAQELDYKVRKYLTDNKQLYTNGPSKYE 168
                                                                                                                                                                                                                                  95 KVKTELLNEDLAKKYKDEVVDVYGSNYYVNCYFSSKDNVGKVTGGKTCMYGGITKHEGNH
                                                                                                                                                                                                                                                         58 KLKTELKNQEMATLFKDKNIDIYGVEYYHLCYLCE-----NAERSACIGGVTNREGNH 110
                                                                                                                                                                                                                                                                                         35 QPDPTPDELHKASKFTGLMENMKVLYDDRYVSATKVKSVDKFLAHDLIYNISDKKLKNYD
                                                                                                                                                                                                                                                                                                                                                 106;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        63 KVKTELLNEDLAKKYKDEVVDVYGSNYYVNCYFSSKDNVGKVTGGKTCMYGGITKHEGNH
                                                                                                                                                                                                                                                                                                                    N
                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                TGYIKFIPKNKESFWFDFFPEP--EFTQSKYLMIYKDNETLDS-NTQIEVYLTTK 220
                                                                                                                                                                                                                                                                                                                  QQDPDPSQLHRSSLVKNL-QNIYFLYEGDPVTHENVKSVDQLRSHDLIYNVSG---PNYD 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TGYIKFIPKNKESFWFDFFPEP--EFTQSKYLMIYKDNETLDS-NTQIEVYLTTK
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                                                                                                                         TGYIKFIENNGNTFWYDMMPAPGDKFDQSKYLMMYNDNKTVDSKSVKIEVHLTTK
                                                                                                                                                                               FUNGKLQNVLIRVYENKRNTISFEVQTDKKSVTAQELDIKARNFLINKKNLYEFNSSPYE
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GITEMBLIEL.
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                                                         PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PubMed=11114901;
                                                                                                                                                                                                                                                                                                                                                        20.6%; Score 516; DB 2; 45.1%; Pred. No. 3.2e-25;
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                                                                                                                                                                                                                                                                                                                                               44;
Created)
Last sequence update)
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Last annotation updat
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Best Local Sim
Matches 106;
STRAIN-MNCOPELAND:
MEDLINE-9401131; PubMed-8406614;
MEDLINE-9401131; PubMed-8406614;
METLIGC, Liyon J D., Roberson J R., Lupher M., Bohach G A.;
"Characterization of novel type C stapphylococcal enterotoxins: blological and avolutionary phyloations.";
Infect: Immun 51:4254-0562 [193] Locations.";
Infect: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE INTOXICATION
STAPHYLOCOCCAL FOOD POISONING STANDAME.
ISSIMIARTY: THE DIFFERENT S. ANERUS ENTEROTOXINS AND S. PYGG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1996 (TREMBLIFEL. 0.1, Created)
01-NOV-1996 (TREMBLIFEL. 0.1 Last sequence update)
01-NOV-1996 (TREMBLIFEL. 0.1 Last annotation update)
Enterotoxin type C (SECOPELAND) (Trengment)
Staphylococcus aureus
Staphylococ
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THE OLIVERASE: STAPHYLOCOCCAL ENTEROTOXIANS CAUSE THE INTOXICATIO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                206533;
                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID-1280;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Staphylococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q06533
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF01123; Stap_Strp_toxin.
Pfam; PF01123; Stap_Strp_toxin; 1.
Pfam; PF02876; Stap_Strp_tox C: 1.
PRINTS; PR00279; BACTRLTOXIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; L13375; AAA26619.1;
HSSP; P34071; 1SE2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-94011313;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-740N:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Staphylococcus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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SIMILARITY: THE DIFFERENT S. ANDREUS ENTEROTOXINS AND S. PYOGENES
PYROGENIC EXOTOXINS ARE ALL RELATED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         169
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TGYIKFIPKNKESFWFDFFPEP--EFTQSKYLMIYKDNETLDS-NTQIEVYLTTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TGYIKFIENNGNTFWYDMMPAPGDKFDGSKYLMWYNDNKTYDSKSVKIEVHLTTK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LEIP--KKIVVKVSIDGIQSLSFDIETNKKMVTAQELDYKVRKYLTDNKQLYTNGPSKYE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KVKTELLNEDLAKKYKDEVVDVYGSNYYVNCYFSSKDNVGKVTGGKTCMYGGITKHEGNH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KLKTELKNQEMATLFKDKNIDIYGVEYYHLCYLCE----NAERSACIGGVTNREGNH 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QPDPMPDDLHKSSEFTGTMDNMKYLYDDHYVSATKVKSVDKFLAHDLIYNISDKKLKNYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QQDPDPSQLHRSS-LVKNLQNIYFLYEGDPVTHENVKSVDQLRSHDLIYNVSG---PNYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               aureus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27642 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      43;
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Pred. No. 3.1e-25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C77009F46BC8D645
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          PYOGENES
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Matches
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Best Local
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Pfam; PF01123; Stap_Strp_toxin; 1.
Pfam; PF0186; Stap_Strp_toxin; 1.
Pfam; PF01876; Stap_Strp_toxin; 1.
Pfam; PF01876; Stap_Strp_toxin; 1.
PROSITE: PS00278; STAPL_STREP_TOXIN_1;
PROSITE: PS00278; STAPL_STREP_TOXIN_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Enterotoxin; Toxin; Superantigen. NON_TER 1 1
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                                                                                                                                                                                                                                           KLKTELKNQEMATLFKDKNIDIYGVEYYHLCYLCE-----NAERSACIGGVTNREGNH 110
                                                         TGYIKFIENNGNTFWYDMMPAPGDKFDQSKYLMMYNDNKTVDSKRVKIEVHLTTK 237
                                                                                               TGYIKFIPKNKESFWFDFFPEP--EFTQSKYLMIYKDNETLDS-NTQIEVYLTTK
                                                                                                                                      FDNGNLQNVLIRVYENKRNTISFEVQTDKKSVTAQELDIKARNFLINKKNLYEFNSSPYE
                                                                                                                                                                                                                  KVKTELLNEDLAKKYKDEVVDVYGSNYYVNCYFSSKDNVGKVTGGKTCMYGGITKHEGNH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      239 AA; 27651 MW;
                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                            20.6%;
                                                                                                                                                                                                                                                                                                                                                                            44;
                                                                                                                                                                                                                                                                                                                                                                                            Score 515; DB 2;
Pred. No. 3.1e-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                      A21A954386AE8625 CRC64;
                                                                                                                                                                                                                                                                                                                                                                            Mismatches
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Query Match Best Local S Matches 107 Stabbylococcus intermedius pyoderma isolates."

Submitted (FEB-1997) to the EMBL/GenBank/DDBJ da

EMBL, 091225, AMB50248.1;

InterPro; IPR001961; Stap/Strep_toxin.

Ffam; PF01123; Stap,Strp_toxin; 1.

Pfam; PF01876; Stap,Strp_toxin; 1.

Pfam; PF01876; Stap,Strp_toxin; 1.

PRAINTS: PR00279; SMCTRLTOXIN.

PROSITE: PS00279; SMCTRLTOXIN.

PROSITE: PS00279; STAPH_STREP_TOXIN.1; 1.

PROSITE: PS00279; STAPH_STREP_TOXIN.2; 1. SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN-95-011195;
Edwards v.M., Deringer J.R., Callantine S.D., Deobald C.F.
Berger P.H., Kapur V., Stauffacher C.V., Bohach G.A.;
Characterization of the type C enterotoxin (SEC-canine)
Characterization of the type C enterotoxin (SEC-canine)
Characterization of the type C enterotoxin (SEC-canine) 01-JUL-1997 (TrEMBLrel. 04, Cr. 01-JUL-1997 (TrEMBLrel. 04, Las 01-MAR-2002 (TrEMBLrel. 20, Las Type C enterotoxin (Fragment). Staphylococcus intermedius. 005157; SEQUENCE NON_TER NCBI_TaxID=1285; Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales; 239 AA; PRELIMINARY; 27536 MW; 20.5%; Score 513; DB 2; Pred. No. 4.1e-25; Pred. No. 4.1e-25; Timmatches 71; Last annotation Last Created Callantine S.D., Deobald C.F., D660644660DE4191 CRC64; sequence update) 239 ₹ update) Length 239; ğ

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QPDPMPDDLHKSSEFTGTMGNMKCLYDDYYVSATKVKSVDKFLAHDLIYNISDKKLKNYD QQDPDPSQLHRSS-LVKNLQNIYFLYEGDPVTHENVKSVDQLRSHDLIYNVSG---PNYD

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Similarity

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Best Local S
Matches 106
                                                                                                                                                                                                                                                                                                                                               PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
Enterotoxin; Toxin; Superantigen.
NON_TER 1.
SEQUENCE 239 AA; 21612 MW; BB7BD62047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MART J.C., LYON J.D., Roberson J.R., Lupher M., Bohach G.A.;
"Characterization of novel type C stabbylococcal enterotoxins:
biological and evolutionary implications.";
Infect. Immun. 61:4254-4626(1993)
-1- DISBASE: STABPYLOCOCCAL EMTEROTOXINS CAUSE THE INTOXICATION
-1- SIMPLACOCCAL FOOD POISONING SYNDROME TRABPICOCCAL FOOD POISONING SYNDROME TO THE DIFFERENT.S. NURSUS EMTEROTOXINS AND S. PYOGENES
                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro: IPR001961; Stap/Strep_toxin.
Pfam: PF01123; Stap_Strp_toxin; 1.
Pfam: PF02876; Stap_Strp_tox_C; 1.
PRINTS; PR00279; BACTRLTOXIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PYROGENIC EXOTOXINS ARE ALL RELATED. EMBL; L13374; AAA26618.1; -. HSSP; P34071; 1SE2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Staphylococcus aureus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NAR-2002 (TREMBLRel. 20, Last anoctation update)
Enterotoxin type C-4 (SEC4446) (Fragment).
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                     169 TGYIKFIPKNKESFWFDFFPEP--EFTQSKYLMIYKDNETLDS-NTQIEVYLTTK 220
                                                                         123
                                                                                   111 LBIP--KKIVYKYSIDGIQSLSFDIETNKKMYTAQELDYKYRXYLTDNKQLYTNGPSKYE 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   169 TOYLKFIPKKKSSFWPDFFEBP-EPTOSKYLMIYKONBYLDS-KMOIKVIJTYK 220
181 TOYLKFIESNONTFWYDMMFAPGDKFDOSKYLMIYSDNKTVDSKSVKIEVHLITIK 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        123 FDNGNLQNVLIRVYENKRNTISFDVQTDXXSVTAQELDIKARNFLINKKNLYEFNSSPYE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              111
                                                                                                                                                                                                                                                                                 106;
                                                                                                                                     63 KVKTELLNEDLAKKYKDEVVDVYGSNYYVNCYFSSKDNVGKVTGGKTCMYGGITKHEGNH
                                                                                                                                                                    58 KLKTELKNQEMATLFKDKNIDIYGVEYYHLCYLCE:----NAERSACIGGVTNREGNH 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               63
                                                                                                                                                                                                                                                                                             Similarity
TGY IKF IENNGNTFWYDMMPAPGDKFDQSKYLMMYNDNKTVDSKSVK IEVHLTTK
                                                                  FDNGNLQNVLVRVYENKRNTISFEVQTDKKSYTAQELDIKARNFLINKKNLYEFNSSPYE
                                                                                                                                                                                                     QPDPHPDDLHKSSEFTGTMGNMKYLYDDHYVSATKVKSVDKFLAHDLIYNISDKRLKNYD 62
                                                                                                                                                                                                                        QQDPDPSQLHRSS-LVKNLQNIYELYEGDPVTHENVKSVDQLRSHDLIYNVSG---PNYD 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LEIP--KKIVVKVSIDGIQSLSFDIETNKKMVTAQELDYKVRKYLTDNKQLYTNGPSKYE 168
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Search completed: June 23, 2003, 16:14:55 Job time: 70.2976 secs

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Result
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          RRPL_RDVA
YE70_METJA
S230_PLAFO
S230_PLAFO
DPOL_CHEPV
V143_NPVAC
RF3_SACBA
Y478_RICPR
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RPOD_MARPO
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RPOD_ASTLO
PPAS_KLULA
Y237_BUCAI
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EMBL; L26126; 
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                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BWE outstation. The Burdenn Bioinformatics Institute on There are no restrictions on its use by non-profit institutions as long as its content is in no way entitled and this statement is not removed. Usage by and for connercial entry entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseeisb-sib.ch).
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the Euro
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MEDIJINE-99386817; PubMed-10.0C.FF. Lei H.-Y., Wu J.-J.;

TBai P.-J., Lin Y.-S., Kuo C.-F., Lei H.-Y., Wu J.-J.;

TBai P.-J., Lin Y.-S., Kuo C.-F., Lei H.-Y., Wu J.-J.;

TGroup A Streptooccus induces apoptosis in human opithelial cells.*;

Infect. Immun. 67:4334-4439(199)

1- FUNCTION: IMPORTANT STREPTOCOCCAL VIRULENCE FACTOR MINICH CLEAVES

HUMAN FIREDRECHESOR TO FORM BIOLOGICALLY ACTIVE TLIB. CAN LYBUCE

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BEDLICES PHAGOCYTIC ACTIVITY IN MONOCITIC CELLS. THUS, MAY DAY A BOLLE IN BACTERIAL COLONIZATION, INVASION, AND INHIBITION OF MOUND

BEDLICES PHAGOCYTIC ACTIVITY IN MONOCITIC CELLS.
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STRAIN=WX131 / Serotype M49,T14;

MEDLINE=99081733; PubMed=9864206;

Muo C.-F., Wu J.-J., Tsai P.-J.,
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MEDLINE-76590087, Pubme-1270417,

Tei J Y., Kortt A.A., Liu T.-Y., Elliott S.D.;

"Primary Structure of streptococcal proteinase.

cyanogen bromide peptides: complete covalent str

polypeptide Chain.;

j. Biol. Chem. 221:1955-1959(1976).
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STRAIN-MASASJ2 / Serotype M18;
STRAIN-MASASJ2 / Serotype M18;
MEDLINE-21927593; PubMed-11317109;
Smoot J.C., Barbian K.D., Van Gompel J.J., Smoot L.M., Chau
Smoot J.C., Sturdevant D.E., Ricklefs S.M., Porcella S.F.,
Sylva G.L., Surdevant D.E., Campbell D.S., Smith T.M., Zhang
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YONAHA K., Elllott S.D., Liu T.-Y.;

"Primary Structure of zymogen of streptococcal
J. Protein Chem. 1:317-334(1982).
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AAA26979.1;
AAA26992.1;
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G -> S (IN STRAIN HGAS 1895).

V -> I (IN STRAIN HGAS 1895).

A -> V (IN STRAIN HGAS 165). 168. 426

659, 660, 79, 800, 1719, 1889. 1889.

2017 AND 2018).

T -> I (IN STRAIN HGAS 650).

T -> I (IN STRAIN HGAS 651).

T -> I (IN STRAIN HGAS 654).

V -> L (IN STRAIN HGAS 664).

V -> L (IN STRAIN HGAS 664).

V -> V (IN STRAIN HGAS 664).

V -> V (IN STRAIN HGAS 664).

I -> V (IN STRAIN HGAS 664).

N -> C (IN STRAIN HGAS 670). STRAIN HGAS 670).

I -> V (IN STRAIN HGAS 1901 AND SV).

S -> G (IN STRAINS A-20, SF370, HGAS 659, 807, 1226, 1719, 1832, 1842, 1846, 1867, 1872, 2017 AND 2018).

A -> S (IN STRAINS HGAS 165, 168, 28

302, 567, 133 AND 1899).

A -> S (IN STRAIN HGAS 1871).

V -> I (IN STRAIN HGAS 1866 AND 1294).

ST -> AS (IN REF. 7).

L -> I (IN REF. 7).
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STRALTH-MGASR322 / Serotype M18;
STRALTH-MGASR322 / Serotype M18;
MEDLINE-2192759; PubMed-11917108;
Smoot J.C., Barbian K.D., Van Gompel J.J., Smoot L.M., Chaussee
Sylva G.L., Sturdevant D.E., Ricklefs S.M., Porcella S.F.,
Sylva G.L., Beres S.B., Campbell D.S., Smith T.M., Zhang Q.,
Kapur V., Daly J.A., Veasy L.G., Musser J.M.;
"Genome sequence and comparative microarray analysis of serotyp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P08055;
01-ANG-1988 (Rel. 08, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
15-UUN-2002 (Rel. 41, Last annotation update)
Exotoxin type A precursor (Scarlet fever toxin) (Erythrogenic toxin)
x-RAY CRYSTALLOGRAPHY (2.57 ANGSTROMS).
MEDLINE-99094887; PubMed-9978045;
Papageorgiou A.C., COllins C.M., Gutman
O'Brien S.M., Tranter H.S., Acharya K.R.
                                                                                                                                                                                                                                                                                                                                                                                                                     "Streptococcal pyrogenic exotoxin type A (scarlet fever related to Staphylococcus aureus enterotoxin B."; Hol. Gen. Genet. 203:354-356(1986).
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"Nucleotide sequence
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                        .M., Gutman D.M.,
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EMBL; A30399; CAA27566.1; ...
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EMBL; A5039982; AAS97441.1; ...
EMBL; A50152; A26152;
ETR; A26152; A26152;
ETR; A26153; A26152;
ETR; ETRO01361; Stap_Strp_toxin; 1...
Fram; PF00123; Stap_Strp_toxin; 1...
FRAUTS; PR00279; ETAPH_STREP_TOXIN_1.1
PROSITE: PS00279; STAPH_STREP_TOXIN_2; 1...
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                                                                                                                                                            CONFLICT
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VSIDGIOSLSFDIETNKKMYTAQELDYKVRKYLTDNKQLYTMOPSKYETGYIKFIPKNKE

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Hunng 1. Y. Bergdoll M.S.;

"The primary structure of staphylococcal
cyanogen broadde peptides of reduced and
B, and the complete amino acid sequence."
J. Biol. Chem. 245:3518-3525(1970).
                                                                                                                                                                                          Li H. Llera A. Tsuchlya D., Leder L., Ysern X., Schlievert Karjalainen K., Kariuzza R.A.; "Three-dimensional structure of the complex between a T cell beta chain and the superantigen staphylococcal enterotoxin B. Immunity 9:807-816(1998).
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Swaminathan S., Furey W.F. Jr., Pletcher J., Sax
Scrystal structure of staphylococcal enterotoxin
                                                                                                                                                                     X-RAY CRYSTALLOGRAPHY (1.5 ANGSTROMS).
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MEDLINE-99096298; Pubmed-9881971;
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MEDLINE-94203282; PubMed-8152483;
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MEDLINE-71007902; PubMed-5470821;
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"Molecular cloning of staphylococcal enterotoxin
Secherichia coli and Staphylococcus aureus.";
Proc. Natl. Acad. Sci. U.S.A. 82:5850-5854(1985).
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MEDLINE-86168029; PubMed-3957869;
Jones C.L., Khan S.A.;
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                                                                                                                                                                                                enterotoxin B.";
                                                                                                                                                                                                                                                                                                                                              HTIW
                                                                                                                                                                                                                                                                                                 D.C.;
histocompatibility
                                                                                                                                                                                                                                                                                                                                                                             B 34
                                                                                                                                                                                                                                                           HTIW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Khan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gene
                                                                                                                                                                                                                                                                                                                         Urban R.G.,
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                                                                                                                                                                                                                                                                                                                                               XX.
                                                                                                                                                                                                                                                                                                                                                                            superantigen.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                    The enterotoxin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     S.A.;
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RESULT 4

ETC3_STAM

ETC3_STAM

DEC3_STAM

REC3_STAM

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Best Local
                                                                                                                                                                                                                                                   01-NOV-1991
01-NOV-1991
15-JUN-2002
Enterotoxin
                                                                                                                                                                                                                                                                                                                                                                       ETC3_STAAM
P23313;
       STRAIN-Mu50 /
                                  SEQUENCE FROM
                                                                                 Staphylococcus aureus
Staphylococcus aureus,
Staphylococcus aureus,
Bacteria; Firmicutes;
NCBI_TaxID=158878, 158
                                                                                                                                                                  Staphylococcus aureus (strain MuSO / Staphylococcus aureus (strain N315),
                                                                                                                                                                                                                        01-NOV-1991 (Rel. 20, Created)
01-NOV-1991 (Rel. 20, Last seque)
15-JUN-2002 (Rel. 41, Last anno
Enterotoxin type C-3 precursor
ENTC3 OR SAV2009 OR SA1817
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CONFLICT
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PIR; /
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or send an
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE: PS00277;
PROSITE: PS00278;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS
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; 2SEB; 28-JAN-98.
; 3SEB; 27-MAY-98.
; 1SE3; 16-JUN-97.
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1SBB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              210
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 QQDPDPSQLHRSSLVKNL-QNIYFLYEGDPVTHENVKSVDQLRSHDLIYNVSGP---NYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ETGYIKPI-ENENSFWYDMMPAPGDKFDQSKYLMMYNDNKMYDSKDVKIEVYLTIKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ETGYIKFIPKNKESFWFDFFPEP--EFTQSKYLMIYKDNETLDS-NTQIEVYLTTKQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GNQLDKYRSITVRVFEDGKNLLSFDVQTNKKKVTAQELDYLTRHYLVKNKKLYEFNNSPY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KLKTELKNOEMATLFKDKNIDIYGVEYYHLCYLCENA------ERSACI-GGVTNRE 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NVRVEFKNKDLADKYKDKYVDVFGANYYYQCYFSKKTNDINSHQTDKRKTCMYGGVTEHN 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QPDPKPDELHKSSKFTGLMENMKVLYDDNHVSAINVKSIDQFLYFDLIYSIKDTKLGNYD
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56
69
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       ATCC
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Signal
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STAPH_STREP_TOXIN_2; 1.
n; Signal; Superantigen;
       700699,
                                                                                     158879,
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                                                                                 Bacillales;
8879, 1280;
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       and N315
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annotation updat
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Y -> YY (IN REF. 3).
QE -> EQ (IN REF. 3).
D -> N (IN REF. 3).
DN -> ND (IN REF. 3).
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MISSING (IN REF.
DIN -> NID (IN RE
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Pred.
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DIN -> NID (IN REF. 3)
QTD -> ENT (IN REF. 3)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ENTEROTOXIN TYPE B
                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -> NND
                                                                                                                Staphylococcus
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                                                                                                                                                                      ATCC 700699), and
                                                                                                                                                                                                                                                                                                                                                                                                   266
                                                                                                                                                                                                                                                                              update)
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.4e-29;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CRC64;
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                                                                                                                                                                      Query Match
Best Local S
Matches 106
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                                                                                                                                                                                                                                                                                                        Interpro; IPROUSO; Stap/Strep_toxin.
Pfam; PPO212; Stap_Strp_toxin; 1.
Pfam; PPO212; Stap_Strp_toxin; 1.
Prim; PPO2876; Stap_Strp_tox; 1.
PRINTS; PRO0279; BACTRLITOXIN.
PROSITE; PS00277; STAPL_STREP_TOXIN_1; 1.
PROSITE; PS00277; STAPL_STREP_TOXIN_2; 1.
Enterotoxin; Toxin; Signal; Superantigen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWI
between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            *Nucleotide sequence of the staphylococcal enterotoxin
                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AP003364; BAB58171.1; -.
EMBL; AP003135; BAB43097.1; -.
EMBL; X51661; CAA35972.1; -.
PIR; S11885; S11885.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nature 384:188-192(1996).
-!- SUBCELLULAR LOCATION: Secreted.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fields B.A., Malchhodi E.L., Li H., Ysern X., Stauffacher C.V., Schilevert P.M., Karjalainen K., Mariuzza R.A.; "Crystal structure of a T-cell receptor beta-chain complexed with a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sequence comparison of all three type C enterotoxins.";
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                                                                                                                                                                                                                                      SEQUENCE
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                                                                                                                                                                                                                                                                                               Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the European Bioinformatics Institute.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DISEASE: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE INTOXICATION STAPHYLOCOCCAL FOOD POLSONING SYNDROME. SINILARITY: BELONGS TO THE STAPHYLOCOCCAL/STREPTOCOCCAL TOXIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bloinformatics and the E
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                                                                                                                                                                        106; Conser
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LEIP--KKIVVKVSIDGIQSLSFDIETNKKMYTAQELDYKVRKYLTDNKQLYTNGPSKYE
                                         KVKTELLNEDLAKKYKDEVVDVYGSNYYVNCYFSSKDNVGKVTGGKTCMYGGITKHEGNH
                                                                        KLKTELKNQEMATLFKDKNIDIYGVEYYHLCYLCE-----NAERSACIGGVTNREGNH
                                                                                                         QPDPMPDDLHKSSEFTGTMGNMKYLYDDHYVSATKVKSVDKFLAHDLIYNISDKKLKNYD
                                                                                                                                   QQDPDPSQLHRSS-LVKNLQNIYFLYEGDPVTHENVKSVDQLRSHDLIYNVSG---PNYD
                                                                                                                                                                                                                                    266
                                                                                                                                                                      Conservative
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tt S.P., Bohach G.A.;
                                                                                                                                                                                                                                                   27
266
137
                                                                                                                                                                                                                                    30671 MW;
                                                                                                                                                                                      20.5%;
                                                                                                                                                                                      Score 513;
Pred. No.
                                                                                                                                                                                                                                                                  ENTEROTOXIN TYPE C-3.
                                                                                                                                                                                                                                    5ED8A32D11FFCA59 CRC64;
                                                                                                                                                                        Mismatches
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5.5e-27;
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                                                                                                                                                                      70;
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                                                                                                                                                                      16;
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                                                                               Pfam; PP01123; Stap_Strp_toxin; 1.
Pfam; PP02P7; Stap_Strp_tox_C; 1.
PRINTS; PR002P7; Stap_Strp_tox_C; 1.
PROSITE: PS002P7; STAPL_STREP_TOXIN_1; 1.
PROSITE: PS002P7; STAPL_STREP_TOXIN_2; 1.
Enterotoxin; Toxin; Signal; Superantigen;
                                                                                                                                                                                                                                                                              Schad E.M., Papageorgiou A.C., Svensson L
A Structural and functional comparison o
enterotoxins A and C2 reveals remarkable
dissimilarity.",
J. Mol. Biol. 269:270-280(1997).
11- COFACTOR: Binds 1 zinc ion per subuni
                                                            SIGNAL
                                                                        3D-structure.
                                                                                                                                                        PIR: A60114; A60114.
PDB: 15TE; 23-DEC-96.
PDB: 15E2; 06-MAR-96.
InterPro; IPR001961; Stap/Strep_toxin.
                                                                                                                                                                                                                   STAPHYLOCOCCAL FOOD
-1- SIMILARITY: BELONGS
                                                                                                                                                                                                                                                        for the toxin interaction with -1- SUBCELLULAR LOCATION: Secreted
                                                                                                                                                                                                                                                                                                                                                       MEDLINE-97334373; PubMed-9191070;
                                                                                                                                                                                                                                                                                                                                                                                                      enterotoxins.
                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-96022987; PubMed-7552730;
Swaminathan S., Furey W.F. Jr., Pletcher
Residues defining V beta specificity in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Crystal structure of the superantigen enterotoxin C2 Staphylococcus aureus reveals a zinc-binding site."; Structure 3:769-779(1995).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
MEDLINE-96027099; PubMed-7582894;
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15-JUN-2002
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P34071;
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                                                                                                                                                                                                                                                                                                                                                                   COMPARISON OF STRUCTURE OF SEA AND
                                                                                                                                                                                                                                                                                                                                                                                           Nat. Struct. Biol. 2:680-686(1995).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Conservation of the biologically active
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bohach G.A., Schlievert P.M.;
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57:2249-2252(1989).
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                                                 ENTEROTOXIN TYPE C-2
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Best Local Sim.
Matches 104;
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Schmidt J.J., Spero L.;
The complete anino acid sequence of staphylococcal enterotoxin Cl.*;
J. Biol. Chem. 258:6300-6306(1983).

1- SUBCELLULAR LOCATION: Secreted.
1- DISEASE: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE INTOXICATION
STAPHYLOCOCCAL FOOD POISONING SYNDROME.
1- SIMILARITY: BELONGS TO THE STAPHYLOCOCCAL/STREPTOCOCCAL TOXIN
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01-JAN-1990
15-JUN-2002
   PROSITE;
                        InterPro; IPRO01961; Stap/Strep_toxin.
Pfam; PF01123; Stap_Strp_toxin; 1.
Pfam; PF02876; Stap_Strp_tox.C; 1.
PRINTS; PR00279; BACTELTOXIN.
                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the Buropean Bioinformatics Institute There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial modified and this statement is not removed. Usage by and for commercials
                                                                                                                                                                                                                                                                                                                                                                                                       Bohach G.A., Schllevert P.M.;
"Nucleotide sequence of the staphylococcal enterotoxin relatedness to other pyrogenic toxins.";
Mol. Gen. Genet. 209:15-20(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Staphylococcus aureus
Bacteria; Firmicutes;
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P01553;
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                                                                                                                                                             entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-83213327;
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STAPH_STREP_TOXIN_1;
STAPH_STREP_TOXIN_2;
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SIGNAL
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CONFLICT
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                                                                                                                                              Kuroda M. Ohta T. Uchiyama I. Baba T. Yuzawa H. Kobayashi
Cui L. Oguchi A. Abaki K. T. Nagai Y. Lian J. O. Ito T.,
Kanamori M., Matsumaru H., Meruyama A., Murekami H. Hoseyama
Mizutani-ti Y. Takahashi N. K. Savano T., Inoue R. H. Joseyama
Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
C. Sawani M., Yamashita N., Oshima K., Furuya K., Yoshino C., S
Mattori M., Osasawara N., Hayashi H., Hiramatsu K.;
                                                                                                                                                                                                                                                                                                                                                                                   Staphylococcus aureus.
Staphylococcus aureus.
Bacteria; Firmicutes; Bacillales;
Bacteria; Firmicutes; 158879, 1280;
                                                                                                                          aureus.
                                                                                                                                                                                                                                    STRAIN-MU50 / ATCC 700699, and N31 MEDLINE-21311952; PubMed-11418146;
                                                                                                                                                                                                                                                                                       "Identification and characterization of staphylococcal enterotóxin types G and I from Staphylococcus aureus."; Infect. Immun. 66:3337-3346(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                         Staphylococcus aureus (strain Mu50 / ATCC 700699), Staphylococcus aureus (strain N315), and
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085382;
                                                                                                                                  "Whole genome sequencing of meticillin-resistant Staphylococcus
                                                                                                                                                                                                                                                              SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                           Munson S.H., Tremaine M.T.,
                                                                                                                                                                                                                                                                                                                                       MEDLINE-98298056; PubMed-9632603;
                                                                                                                                                                                                                                                                                                                                                     STRAIN-FRI572
                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A., AND PARTIAL SEQUENCE
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15-JUN-2002 (Rel. 41,
15-JUN-2002 (Rel. 41,
                                                       SUBCELLULAR LOCATION: Secreted.
DISBASE: STAPHYLOCOCCAL ENTEROTIXINS CAUSE THE INTOXICATION STAPHYLOCOCCAL FOOD POISONING SYNDROME.
SIMILARITY: BELONGS TO THE STAPHYLOCOCCAL/STREPTOCOCCAL TOXIN
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                                                                                                                                                                                                                                                                                                                             Welch R.A.;
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Best Local Similarity
Matches 101; Conser
STRAIN-ATCC 53977;
MEDILINE-95105001; PubMed-7806362;
Madden T. E. (Clark V.L., Kuramitsu H.K.;
Madden T. E. (Clark V.L., Kuramitsu H.K.;
Madden T. E. (Clark V.L.)
Medden T. 
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PRTT_PORGI
                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-93114862; PubMed-8093357;
Octogoto J.-I., Kuramitsu H.K.;
"Isolation and characterization of the Porphyromonas gingivalis gene, coding for protease activity.";
Infect. Immun. 61:117-123(1993).
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01-NOV-1995
                                                                                                                                                                                                                                                                                                                                 REVISIONS, SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-ATCC 53977;
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Pfam; PF02876; Stap_Strp_tox_C; 1.
PR0SITE; PS00277; STAPH_STREP_TOXIN_1;
PR0SITE; PS00278; STAPH_STREP_TOXIN_2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (Rel. 32, Created)
(Rel. 32, Last sequence update)
(Rel. 32, Last annotation update)
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Pred. No. 2.1e-22
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Best Local (
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01-FEB-1991
15-JUN-2002
                                                                                                                                                                     enterotoxin D.
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ACT_SITE
SEQUENCE
                                                                                                                                    J. Bacteriol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ENTD
                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=1280;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P20723;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   468
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SEQUENCE FROM N.A., AND X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).
  MEDLINE-97157473;
                                                                                                                         SEQUENCE FROM N.A.
MEDLINE=89359112; PubMed=2549000;
                                                                                                                                                                                      Staphylococcus aureus
Bacteria; Firmicutes;
                                                                                        Bayles K.W., Iandolo J.J.;
"Genetic and molecular analyses of
                                                                                                                                                                                                                                      Enterotoxin type D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseeisb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR000200; Peptidase_C10.
InterPro; IPR001230; Prenyl_site.
Pfam; PF01640; Peptidase_C10; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBL outstation . The European Bioinformatics institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; M83096; -; NOT_ANNOTATED_CDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C10.
-- CAUTION: IT IS UNCERTAIN WHETHER MET-1 OR MET-17 IS THE INITIATOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEROPS; C10.002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         230 SKGIHYNQGNPYNLLTFVIEKVKPGEQSFVGQHAATGCVATATAQIMKYHNYPNKGLKDY 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                701640; Pep......
PR00797; STREEPTOPAIN.
se; Thiol protease; Signal; Hemagglutinin.
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                          DGSMGHAFVCDGYEPDGTFHFNWGWGGMSNGNFYLNLLNPGSLGTGAGDGGYSTDQEVVI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KVG-GHAFVIDGADGRNFYHVNWGWGGVSDGFFRIDAINPSALGTGGGAGGFNGYQSAVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DYGPSSGSAGSSRVQRALKENFGYNQSVHQINRSDF-SQDWEAQIDKELSQNQPVYYQGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYTLSSNNPYFNHPKNLFAAISTRQYNWNNILPTYSGRESNVQKMAISELMADVGISVDM
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                                                                                                                                                                                                                                                        (Rel.
(Rel.
(Rel.
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                                                          171:4799-4806(1989).
                                                                                                                                                                                                                                                                                                                     STANDARD;
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184
327
96444
PubMed-9003758,
                                                                                                                                                                                                                                                        41,
                                                                                                                                                                                                                                                                     17,
                                                                                                                                                                                                                                      precursor (SED).
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                                                                                                                                                                                                                                                   Last sequence up
                                                                                                                                                                                                                                                                                   Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16.9%; Score 422;
39.0%; Pred. No. 3
                                                                                                                                                                                         Bacillales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MW;
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THIOL PROTEASE/HEMAGGLUTININ
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   45436EFE32779323 CRC64;
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                                                                                                                                                                                    Staphylococcus
                                                                                            the
                                                                                                                                                                                                                                                   on update)
                                                                                                                                                                                                                                                                                                                  258
                                                                                          gene
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                                                                                     encoding staphylococcal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Length 868
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         467
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ETXA_STAM
ID ETXA_S
AC P13163
DT 01-XM
DT 15-JDM
DE Enterc
GN ENTA C
GN Staphj
OS Staphj
OS Staphj
OS Staphj
OS Staphj
OS NCBL-;
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Best Local S
Matches 79
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HSSP: P13163; LSXT;
InterPro: IPRO01961; Stap/Strep_toxin.
Pfan: PP01123; Stap_Strp_toxin; 1.
Pfan: PP01123; Stap_Strp_toxin; 1.
Pfan: PP02076; Stap_Strp_toxin; 1.
PRINTS: PR00279; Stap_Strp_toxin; 1.
PR051TE; P800279; STAPH_STREP_TOXIN_1; 1.
PR051TE; P800279; STAPH_STREP_TOXIN_1; 1.
                                                               01-JAN-1990 (Rel. 13
01-JAN-1990 (Rel. 13
15-JUN-2002 (Rel. 41
Enterotoxin type.A F
ENTA OR MW1889
                                                                                       ETXA_STAAW
P13163;
01-JAN-1990
01-JAN-1990
15-JUN-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         METAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Zn2+-mediated homodimerization.";
EMBO J. 15:6832-6840(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sundstroem M., Abrahmsen L., Antonsson P
Dohlsten M.;
"The crystal structure of staphylococcal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ÷
                                       Staphylococcus aureus (strain MW2), Staphylococcus aureus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Enterotoxin;
             NCBI_TaxID-196620,
                           Bacteria; Firmicutes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBBLIT: HOMODINÉR: ZÎMC-DEPENBEN:
SUBCELLÎLAN LOCATION: SOCICE OF
DISEASE: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE INTOXICATION
STAPHYLOCOCCAL FOOD POISONING SYNDROME.
STAPHYLOCOCCAL FOOD POISONING SYNDROME.
STAPHYLOCOCCAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FAMILY
                                                                                                                                                                                                                213
                                                                                                                                                                                                                                                                   153
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                               TELKNQEMATLFKDKNIDIYGVEYYHLCYLCENAERSAC-IGGYTNREGNHLBIPKKIVV
                                                                                                                                                                                                                                                                                                                                                                                                     QLHR-----SSLVKNLQNIYFLYEGDPVTHENVKSVDQLRSHDLIYN----VSGPNYDKLK
                                                                                                                                                                                                                               PKNKESFWFDFFPEPEFTQSKYLMIYKDNETLDS-NTQIEVYLTTK
                                                                                                                                                                                                                                                                                                                       INFNSKEMAQHFKSKNYDYYPIRYSINCYGGE-IDRTACTYGGYTPHEGNKLKERKKIPI
                                                                                                                                                                                                                                                                                                                                                                           ELHKKSELSSTALNNMKHSY--ADKNPIIGENKSTGDQFLENTLLYKKFFTDLINFEDLL
                                                                                                                                                                                                                SSDGSKYSYDLFDYKGDFPEKQLRIYSDNKTLSTEHLHIDIYLYEK
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Toxin;
                                                                                                                                                 STANDARD;
                                                                                           13, Created)
13, Last sequence up
41, Last annotation
                                                                                precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Signal; Superantigen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29746 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                           11.8%;
                             Bacillales; Staphylococcus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                44;
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ZINC.
ZINC.
ZINC.
P -> A (IN STRAIN AT
                                                                                                                                                                                                                                                                                                                                                                                                                                             Score
Pred.
                                                                                (SEA)
                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -> A (IN STRAIN ATCC 23235).
4F7C6A28D42597FD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
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                                                                                             on update)
                                                       and
                                                                                                                                                   257
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                                                                                                                                                                                                                                                                                                                                                                                                                                             2e-12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                   ; 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 258;
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                                                                                                                                                                                                                                              220
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Baba T. Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguch.
Nagai Y., Irama N., Asano K., Naimi T., Kuroda H., Cui L.,
Yamamoto K., Hiramatsu K.;
'Genome and virulence determinants of high virulence community
acquired MRSA.'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Schad E.M., Papageorgiou A.C., Svensson L.A., Acharva K.R. A structural and functional comparison of staphylococcal enterotoxins A and C2 reveals remarkable similarity and dissimilarity. Service of the standard of the stan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 X-PAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).

MEDLINE-95354648; Pubmed-7628431;
Schad E.M., Zaltseve V.N., Dohlsten M.,
Schlievert P.M., Ohlendorf D.H., Svensson L.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-8722293; PubMed=3584106;
NLang 1.-Y., Hughes J.L., Bergdoll M.S., Schantz E.J.;
Topplete amino acid sequence of staphylococcal enterotoxin
J. Biol. Chem. 262:7006-7013(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 25-257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Betley M.J., Mekalanos J.J.;
*Nucleotide sequence of the type A staphylococcal enterotoxin gene.*;
J. Bacteriol. 170:34-41(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-22040717; PubMed-12044378;
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STRAIN-MW2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            zn2+ at 2.7-A resolution. Implication
complex class II binding.";
J. Biol. Chem. 271:32212-32216(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS)
MEDLINE-97113025; PubMed-8943278;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-88086892; PubMed-3335483;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lancet 359:1819-1827(2002).
                                                 use by non-profit institutions as long modified and this statement is not removed entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPARISON OF STRUCTURE OF SEA AND SEC2
MEDLINE-97334373; PubMed-9191070;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Swaminathan S., Furey W.F. Jr., Pletch
"Residues defining V beta specificity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "The Co-crystal structure of staphylococcal zn2+ at 2.7-A resolution. Implications for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sundstroem M., Hallen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBO J. 14:3292-3301(1995).
                                                                                                                                                       This SHISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMBL outstation. the European Bioinformatics institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                  -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nat. Struct. Biol. 2:680-686(1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 enterotoxins.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Abrahmsen L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   *Crystal structure of the superantigen staphylococcal enterotoxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3D-STRUCTURE MODELING
                                                                                                                                                                                                                                                                                               for the toxin interaction with MHC class II.

SUBRUIT; MONDER, ASSET OF THE STATEMENT OF THE INTOXICATION

DISEASE: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE INTOXICATION

STAPHYLOCOCCAL END POISONING STAPHYLOCOCCAL FOOD POISONING STAPHYLOCOCCAL FOOD FOR THE STAPHYLOCOCCAL/STREPTOCOCCAL TOXIN

SIMILARITY: BELONGS TO THE STAPHYLOCOCCAL/STREPTOCOCCAL TOXIN
                                                                                                                                                                                                                                                                            FAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pletcher
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     subunit. The zinc MHC class II.
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Kuroda H., Cui L.
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                                                                                   http://www.isb-sib.ch/announce/
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EMBL; AP004628; BAB95754.1;

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SUBCELIULAR LOCATION: Secreted.
DISEASE: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE INTOXICATION
STAPHYLOCOCCAL FOOD POISONING SYNDROME.
SIMPLARITY: BELONGS TO THE STAPHYLOCOCCAL/STREPTOCOCCAL TOX.

TOXIN

FAMILY.

This SRISS-PROT entry is copyright. It is produced through a collaboration between the SRIss institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its

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RESULTANT PROPERTY OF TAXABLE STREET PROPERTY OF
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Matches 70
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01-JAN-1990
15-JUN-2002
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Prim: PPO11212: Stap_Strp_toxin. 1.

Prim: PP01212: Stap_Strp_tox. C: 1.

PRIM: P002121: Stap_Strp_tox. C: 1.

PRIM: P002121: STAPLETREP_TOXIN. 1: 1.

PROSITE: P002121: STAPLETREP_TOXIN. 1: 1.

Encertoxin: Toxin: Stapletrep_toxin. 1: 1.

Encertoxin: Toxin: Stapletrep_toxin. 1: 1.

Encertoxin: Toxin: Stapletrep_toxin. 1: 1.
                      Nat. Struct. Biol. 2:680-686(1995)
-1- COFACTOR: Binds 1 zinc ion per
                                                              enterotoxins.";
                                                                         MEDLINE 96022987; PubMed 7552730;
Swaminathan S., Furey W.F. Jr., Pletcher
Residues defining V beta specificity in
                                                                                                                                                                               "Cloning and nucleotide sequence of enterotoxin gene.";
J. Bacteriol. 170:2954-2960(1988).
                                                                                                                                                                                                                                             Couch J.L.,
                                                                                                                                                                                                                                                                                       STRAIN-MJB265;
                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A., AND SEQUENCE OF
                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Firmicutes;
                                                                                                                                                                                                                                                                                                                                                                                       Staphylococcus aureus
                                                                                                                                                                                                                                                                                                                                                                                                                                  Enterotoxin
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                                                                                                                                                                                                                                                              MEDLINE-88257005; PubMed-3384800;
                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=1280;
                                                                                                                                             3D-STRUCTURE
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1SXT; 19-NOV-97.
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1ESF; 11-JUL-9
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  the toxin
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13, Last sequence update)
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  interaction v
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subunit. The MHC class II
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                                                                               J., Sax M.;
staphylococcal
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                   is necessary
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RESULT 12
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SPEH_STRPY
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AC 0X564
AC 0X56
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16-OCT-2001 (Rel. 40, Last s
15-JUN-2002 (Rel. 41, Last a
Exotoxin type H precursor (S
SPEH OR SPY1008.
                                                                                                                                                                                                                                                                                                                                                                   SPEH_STRPY
Q9X5C8;
16-OCT-2001
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PDB, 1SEE, 15-COT-95,
InterPro, IPROM1961, Stap/Strp_Loxin, 1,
Pfam, PF01323, Stap_Strp_Loxin, 1,
Pfam, PF02876, Stap_Strp_Lox.C, 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
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Bacteria; Firmicutes;
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rsor (SPE H).
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                                                                                                                                                                                                                       Lactobacillales; Streptococcaceae;
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ZINC (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 256.5; DB 1
Pred. No. 4.2e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
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                                                                                                                                                                                                                                                                                                                       update)
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MEDLINE-99093428; PubMed-9874566; Proft T., Moffatt S.L., Berkahn C.J. "Identification and characterization

of

novel superantigens from

Fraser J.D.;

STRAIN-MI

SEQUENCE FROM N.A.

Streptococcus pyogenes.";

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RESULT 13
SPEC_STRPY
ID SPEC_F
AC P1338
DT 01-J
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DT 16-OC
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OS Strep
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Best Local S
Matches 67
                                                              SPEC_STRPY STANDARI
P1380;
01-JAN-1990 (Rel. 13, 0
16-OCT-2001 (Rel. 40, 1
16-OCT-2001 (Rel. 40, 1
            Bacteria; Firmicutes; Streptococcus.
                              Exotoxin type C precursor SPEC OR SPY0711.
Streptococcus pyogenes.
                                                                                                                         STRPY
                                                                                                                                                                                                                                                                                                                                                                                                                            Interpro: IPROUJS61; Stap/Strep_toxin.
Interpro: IPROUJS61; Stap_Strp_toxin; 1.
Pfam: PF01123; Stap_Strp_toxin; 1.
Pfam: PF02176; Stap_Strp_toxin; 1.
PROSITE: PS00277; STAPE_STREP_TOXIN; 1;
PROSITE: PS00278; STAPH_STREP_TOXIN, 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the European Bioinformatics Institute, There are no restrictions of its use by non-profit institutions as long as its content is in no way modified and this statement is not removed, Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AF124500; AAD30989.1; -. EMBL; AE006546; AAK33907.1; -. HSSP; P13163; 1SXT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       or send an e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ferretti J.J., McShan H.M., Ajdic D.J., Savic D.J., Savic G., Lyon K., Primenux C., Sezate S., Suvorov A.N., Kenton S., Lai H.S., Lin S.P., Qian Y., Jia H.G., Najar F.Z., Ren Q., Zhu H., Song L., White J., Yuan X., Clifton S.W., Roe B.A., McLaughlin R., "Complete genome sequence of an M strain of Streptococcus pyogenes."; Proc., Natl., Acad., Sci. U.S.A., 98:4658-4663(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                      Toxin; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a c
between the Swiss Institute of Bioinformatics and the EMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-SF370 / ATCC 700294 / Serot
MEDLINE-21192684; PubMed-11296296;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.
 _TaxID=1314;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBCELUIAR LOCATION: Secreted:
DISEASE: MICOGRAFIC human peripheral blood lymphocytes.
SIMILARITY: BELONGS TO THE STAPHYLOCOCCAL/STREPTOCOCCAL TOXIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBUNIT: Binds to major histocompatibility complex
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                                                                                                                                                                                                                                                                                                                                             67;
                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Med. 189:89-102(1999).
                                                                                                                                                                  DF -- NSMLKIYSNNERIDS-TQFHV
                                                                                                                                                                                        EFTOSKYLMIYKDNETLDSNTQIEV
                                                                                                                                                                                                                      IETNKKMVTAQELDYKVRKYLTDNKQLYTNGPSKYETGYIKFIPKNKESFWFD--FFFEP
                                                                                                                                                                                                                                                     KEVDIYALSAQEVCE-CP-GKRYEAFGGITLTNSEKKEIKVP----VNVWDKSKQQPPMF
                                                                                                                                                                                                                                                                        KNIDIYGVEYYHLCYLCENAERSACIGGV--TNREGNHLEIPKKIVVKVSIDGIQSLSFD
                                                                                                                                                                                                                                                                                              NRHNLESLYKHDSNLIEADSIKNSPDIVTSHMLKYSVKDKN----LSVFFEKDWISQEFKD
                                                                                                                                                                                                                                                                                                                 NLONIYFLYEGDP--VTHENVK-SVDQLRSHDLIYNVSGPNYDKLKTELKNQEMATLFKD
                                                                                                                                                                                                          ITVNKPKVTAQEVDIKVRKLLIKKYDIYNNREQKYSKGTVTLDLNSGKDIVFDLYYFGNG
                                                                                                                                                                                                                                                                                                                                                                                      236 AA;
                                                                                                                                                                                                                                                                                                                                           Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                             Complete proteome.
1 32 POTE
                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                   236 E
; 27485 MW;
                                                                                                                                                                                                                                                                                                                                                    8.1%;
                                                              Last sequence update)
                   Lactobacillales; Streptococcaceae;
                                                                                      Created)
                                                     (SPE
                                                                                                                                                                                                                                                                                                                                           29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         / Serotype
                                                                                                                                                                                                                                                                                                                                                   Score 203.5;
Pred. No. 1.1
                                                                                                                                                                                                                                                                                                                                                                                   EXOTOXIN TYPE H.
16352923907AD40D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                          POTENTIAL
                                                     9
                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                  231
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                                                               update:
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                                                                                                                                                                                                                                                                                                                                                              DB 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                collaboration
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              outstation
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                   CONFLICT
                                                  SIGNAL
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STRAIN-T18P / MGAS
                                                                                                                                                                                                                                                                                                        FAMILY.
               28
53
235
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Roussel A., Anderson B.F., Baker H.M., Fraser J.D., Baker E.N.; Crystal structure of the streptococcal superantigen SPE-C: dimenization and zinc binding superat a novel mode of interacti with MHC class II molecules.", Nat. Struct. Bol. 4:635-643(1997).

Nat. Struct. Bol. 4:635-643(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           *Molecular population genetic evidence of horizontal alleles of the pyrogenic exotoxin C gene (spec) among clones of Streptococcus pyogenes.";
Infect. Immun. 60:3513-3517(1992).
This SMISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bloinformatics and the EMBL outsu the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for con
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ferretti J.J., McShan M.M., Ajdic D.J., Savic D.J., Savic Primeaux C. Sezate S., Suvorov A. N., Kenton S., Li H.S., Olan Y., Jia H.G., Majar F.Z., Ran Q., Zhu H., Song L., Wh Yuan X. Clifton S.H., Roe B.A., McLaughlin R., Tomplere genome sequence of an M. Strain of Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-SF370 / ATCC 700294 / Serotype M1; MEDLINE-21192684; PubMed-11296296;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-92363541; PubMed-1500157; Rapur V., Nelson K., Schlievert P.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Goshorn S.C., Schlievert P.M.;
"Nucleotide sequence of streptococcal
Infect. Immun. 56:2518-2520(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (1)
SEQUENCE FROM N.A., AND SEQUENCE STRAIN-TIME / MGAS 1585;
MEDLINE-88314303; PubMed-1045005;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS)
MEDLINE=97397352; PubMed=9253413;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Proc. Natl. Acad. Sci. U.S.A. 98:4658-4663(2001).
                                                                                                                                                                                                     FEVER.
MISCELLANEOUS: THIS
SIMILARITY: BELONGS
                                                                                                                                                                                                                                                                                      DISEASE: THE STREPPOCOCCAL PYROGENIC TOXINS A, B, AND C ARE THE CAUSATIVE AGENTS OF THE SYMPTOMS ASSOCIATED WITH SCALED FOR STREPPOCOCCAL TOXIC SHOCK-LIDISEASE AND MAY PLAY A ROLE IN THE EARLY EVENTS OF RHEUMATIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MGAS 1585;
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                                                                                                                                                                                                     TOXIN SEEMS TO BE CODED BY A BACTERIOPHAGE TO THE STAPHYLOCOCCAL/STREPTOCOCCAL TOXIN
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Lai H.S., Li
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spread of two
pathogenic
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                                                                                                                                                                                                                                                                                                                          SCARLET
SHOCK-LIKE
                                                                                                                    a collaboration
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for commercial
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PIR: A30509; A30509.

PDB: IANN; 29-APR-98.
INTERPRO: IPROCU961; Stap/Strep_toxin.
PFAm; PF021123; Stap_Strp_toxin; 1.
PFAm; PF021124; Stap_Strp_tox.C; 1.
PFAm; PF02179; BACTRLTOXIN. PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
TOXIN; Signal; 3D-structure; Complete proteome. EMBL; M35514; AAA27017.1; ALT_SEQ. EMBL; M97156; AAB59091.1; -EMBL; M97157; AAB59092.1; -EMBL; AE006523; AAK33664.1; -27371 **Ξ** N -> D (IN REF. 070534ABB952C1E0 CRC64;

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PROGRESSING STRATION OF STRATI
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16-CCT-2001 (Rel. 40, Creat
16-CCT-2001 (Rel. 40, Last
16-CCT-2001 (Rel. 40, Last
16-CCT-2001 (Rel. 40, Last
Exctoxin type G precursor (
SPEG OR SPY0212.
                                                                                              EMBL; AF124499; AAD30988.1; -.
EMBL; AE006489; AAK33303.1; -.
EMBL; AE006489; AAK33303.1; -.
HSSP; P13380; IANB
InterPro; IPR001961; Stap/Strep_toxin.
                                                                                                                                                                                                            the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (see http://www.isb-sib.ch/anor send an email to license@isb-sib.ch).
                         Pfam; PF01123; Stap_Strp_toxin; 1.
Pfam; PF02876; Stap_Strp_tox_C; 1.
PRINTS; PR00279; BACTRLTOXIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ferretti J.J., McShan W.M., Ajdić D.J., Savic D.J., Savic G., Primeaux C., Serate S., Suvorova A.N., Kenton S., Lail H.S., G., Olan Y., Jia H.G., Najar F.C., Ren G., Zhu H., Song L., White Yuan X., Clifton S.W., Barbara A., McLaudhiln R., Song L., White Yoan X., Clifton S.W., Savic B.A., McLaudhiln R., Song L., White Yoan X., Clifton S.W., Savic B.A., McLaudhiln R., Song L., White Young Complete genome sequence of an M. Strain of Streptococcus py Proc. Natl., Acad. Sci. U.S.A., 88:4658-4651(2001).
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Proft T. Mcffatt S.L. Berkahn C.J.,
"Identification and characterization of
Streptococcus pyogenes."
J. Exp. Med. 189:89-102(1999).
                                                                                                                                                                                                                                                                                                                                                                     between
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Bacteria; Firmicutes; I
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DISEASE: Mitogenic for SIMILARITY: BELONGS TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  chain.
                                                                                                                                                                                                                                                                                                                                                          SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the Ev
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Best Local
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SEQUENCE
                                                                 SEQUENCE OF 181-190; 314-328; 366-377; 420-430; 494-506; 661-677; 900-914 AND 105-1077.

HEXTMAN V. HEXTMAN J., KIST M.;

SUBMITTED (APR-1993) to the SWISS-PROT data bank.

-1- FUNCTION. HAY BE NECESSARY FOR THE TRANSCRIPTION, FOLDING, E) OR FUNCTION OF THE CITOTOXIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          P80200;
01-007-1995 (Rel. 34, Created)
01-007-1995 (Rel. 34, Last sequence update)
15-UNY-2002 (Rel. 41, Last annotation update)
                                                                                                                                                              Censini S., Lange C., Xiang Z., Crabtree J., Ghiara Borodovsky M., Rappuoll R., Covacci A., "eag, a pathogenicity island of Helicobacter pylori, specific and disease associated virulence factors.";
                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN-CCUG 17874 / NCTC 11638;
MEDLINE-93296225; PubMed-8516329;
                                                                                                                                                                                                              MEDLINE-97121442;
                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN-CCUG 17874 / NCTC 11638;
                                                                                                                                                                                                                                                              Proc. Natl. Acad.
                                                                                                                                                                                                                                                                                   "Molecular characterization of
Helicobacter pylori associated
                                                                                                                                                                                                                                                                                                           Rappuoli R.;
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Macchia G., Massone
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Toxin; Signal; Complete proteome.
SIGNAL 1 24 POTENTIAL
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27262 MW;
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A., Papini E.,
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InterPro; IFR005169; CagA.
InterPro; IFR004355; IVSec_cagA.
Pfam; PF03507; CagA; 1.
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443 DALN--PSALGTGGGAGGF 459
                                                                      874 AKLGNENNNNNNGLKNEPIYAKVNKKKAGQAASLEEPIYAQVAKKVN------AKI 923
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   694 LKDFDKSFDEFKNGKNKDFSKAEETLKALKGSVKDLGINPEWISKVENLNAALNEFKNGK 753
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     286 LKDYTYT-----R 313
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                                                                                                                                                                                                           SKEQLAQQAQKNESLNARKKSEIYQSVKNGVNGTLVGNGLSQAEATTLSKNFSDIKKELN 873
                                                                                                                                                                                                                                                                                                                                                                                                       QYNWNNILPTYSGRESNVQKMAISELMADVGISVDMDYGPSSGSAGSSRVQRALKE--NF 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PYNLLTPVIEKVKPGEQ-----SFVGQHAATGCVATATAQIM------KYHNYPNKG 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LPDL----NNLAITS-----FVRRNLED--KLTTKGLSPQEANKLIKDFLSSNKELVG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NVTLQCSLKHDGVMFVDYSNFKY--TNASKNPNKGVGVTNGV-SHLEVGFN---KVAIFN 539
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                                                                                                                                                                                                                                                                        G------AQIDKELS 398
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                                                                                                                                        -----QNQPVYYQGG--KVGGHAFVIDGADGRNFYHVNWGWGGVSDGFFRL 442
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19.4%; Pred. No. 1.8;
vative 97; Mismatches 184; Indels 218;
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924

DRLNQIASGLGVVGQAAGF 942

Search completed: June 23, 2003, 16:13:02 Job time: 20.2253 secs

GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

June 23, 2003, 16:10:06; Search time 34.4979 Seconds (without alignments)
1304.163 Million cell updates/sec

Run on:

Title: . Perfect score: US-10-002-784A-27 2500 MQQDPDPSQLHRSSLVKNLQ.....ALGTGGGAGGFNGYQSAVVG 468

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5

283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters:

283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database PIR_73:* pir1:*
pir2:*
pir3:*
pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result

Query

probable flagellin	G81361	N	750	5.0	124.5	29
1ca1	DR9807	٠,	231	ري س ز	132.5	28
_	H82885	s K	2500	ло л k	177	27
enterotoxin Yentl	В89969	N	133		164 F	7 0
exotoxin C precurs	A30509	· N	235		183	2 4
	C89969	N	242	8.7	218	2 6
enterotoxin SEM	D89969	N	239	9.5	237.5	4 6
	A28179	N	257	10.3	256.5	2 2
	A28664	N	257	10.3	257.5	20
enterotoxin SeN	нв996в	N	258	10.5	262.5	19
ρ	G89991	N	240	10.5	263	18
	C89984	ພ	. 260	11.2	279.5	17
	E89969	N	260	11.7	291.5	16
enterotoxin D prec	A33953	N	258	11.8	295.5	: 5
enterotoxin YENT2	A89969	N	136	12.1	303.5	, L
cysteine proteinas	T10890	N	886	16.9	422	13
	G89968	N	258	17.8	444	12
	ENSAC1	_	266	20.4	509	: =
	A60114	N	266	20.4	510	10
	S11885	N	266	20.5	513	٠
enterotoxin B	ENSAB6	<u></u>	266	21.6	541	œ
ဂ္ဂ	A26152	<u>,_</u>	250	37.5	938.5	7
	S18789	2	236	39.5	986.5	0
	S18786	N	236	43.6	1089.5	u
	S18783	N	236	43.9	1096.5	4
	S29659	_	251	45.2	1129	. (
streptopain (EC	BPSOP	_	337	47.9	1198	
streptococcal	A37768	N	398	53.1	1327.5	_
Description	Ą	DB	Length	Match	Score	No.

116.5 116.5	117 117 116.5	119	122.5	123 123 122.5	124.5 123.5
4.7	4.7	4 4 4	444	444	4.9
824 840	675 1186 770	351 1306	1146 1881 378	227 1215 960	1183
NN	222	222	0000	222	22
A48910 137281	S16624 C64588 B48910	T285/6 D89991 T28313	A89922 H95076 AD1541	C89808 B48281 S72284	F90559 G82885
desmocollin la pre Dscla precursor -	<pre>penicillin-binding cag pathogenicity desmocollin lb pre</pre>	<pre>rhoptry protein - hypothetical prot ORF MSV152 probab</pre>	<pre>conserved hypothet zinc metalloprotet hypothetical prote</pre>	exotoxin 15 [import cytotoxin-associated DNA-directed RNA p	conserved hypothet

ALIGNMENTS

A37	ŝ
768	
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streptococcual pyrogenic exotoxin type B precursor - Streptococcus pyogenes C;Species: Streptococcus pyogenes C;Species: Streptococcus pyogenes C;Date: Jl.May-1991 Sequence_revision 31-May-1991 *text_change 22-Jun-1999 C;Accession: A37768 R;Hauser, A.R.; Schlaevert, P.M. J. Bacteriol. 172, 4536-4542, 1990 A;Title: Nutlocide sequence of the streptococcal pyrogenic exotoxin type B gene and A;Reference number: A37768; MUID:90330563; PMID:2198264 A;Accession: A37768; MUID:90330563; PMID:2198264 A;Accession: A37768; MUID:90330563; PMID:2198264

A; Molecule type: DNA A; Residues: 1-398 <HAU>

A;Cross:references: GB:M86905; GB:M35110; NID:g153818; PIDN:AAA26978.1; PID:g153819 C:Superfamily: Streptococcal cysteine proteinase C:Keywords: exotoxin

Db	νQ	Db	Qγ	망	Qy	ф	Qy	Ф	Qy	Matche	Query Match Best Local
354 HVNWGWGGVSDGFFRLDALNPSALGTGGGAGGFNGYQSAVVG 395	427 HVNWGWGGVSDGFFRLDALNPSALGTGGGAGGFNGYQSAVVG 468	294 ENFGYNQSVHQINRSDFSKQDWEAQIDKELSQNQPVYYQGVGKVGGHAFVIDGADGRNFY 353	369 ENFGYNQSVHQINRSDFS-ODWEAQIDKELSQNQPVYYYGG-GKVGGHAFVIDGADGRNFY 426	234 AISTROYNMUNILPTYSGRESNVQKMAISELMADVGISVDMDYGPSSGSAGSSRVQRALK 293	309 AISTROYNWNNILPTYSGRESNVQKMAISELMADVGISVDMDYGPSSGSAGSSRVQRALK 368	174 EKVKPGEQSFVGQHAATGCVATATAQIMKYHNYPNKGLKDYTTTLSSNNPYFNHPKNLFA 233	249 EKVKPGEQSFVGOHAATGCVATATAQIMKYHNYPNKGLKDYTYTLSSNNPYFNHPKNLFA 308	120 FMES-YVEQIKENKKLDTTYAGTAEIKQPVVKSLLDSKGIHYNQGNPYNLLTPVI 173	IOI		Query Match 53.1%; Score 1327.5; DB 2; Length 398; Best Local Similarity 91.5%; Pred. No. 1.4e-79;

RESULT 2

BPSOP

Streptopain (EC 3.4.22.10) precursor - Streptococcus pyogenes

N;Alternate names: streptococcal cysteine proteinase; streptococcal peptidase A

C;Species: Streptococcus pyogenes

C;Date: 74.Apr-1984 #sequence_revision 07-Oct-1994 #text_change 07-Oct-1994

C;Accession: S07668; A00978

R;Yonaha, K; Elliott, S.D.; Liu, T.Y.

J. Protein Chem. 1, 317-334, 1982

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RESULT 3

299530

AND THE PROCESS OF THE PROCESS PROGENES PROGENES
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A: Accession: 807668

A: Noiseaute type: protein A: Residues: 1-39 70014

R: Tail J Y Y: Kortt. A.A.: Liu, T.Y.: Elliott, S.D.
J. Biol. Chem. 251, 1955-1959, 1976

A: Title: Primary structure of streptococcal proteinase. III. 180

A: Reference number: A00978; MUID: 78190087; PMID:1270417

A: Accession: A00978

A: Molecule type: protein
A: Noiseaute: 85-107, L',109-244, 'N', 246-337 <AIY
A: Noiseaute: 85-107, L',109-244, 'N', 246-337 <AIY
A: Noiseaute: Type: protein
A: Noiseaute: S9-107, L',109-244, 'N', 246-337 <AIY
A: Noiseaute: S9-107, L',
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EMBL Data Library, September 1991
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                          RESULT 4
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STATE THE A PRECURSOR (allele 3) - Streptococcus
RyAlternate names: scarlet fever toxin
RyAlternate: Streptococcus pyogenes phage
C;Species: Streptococcus pyogenes phage
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A: MALGOLLE type: DNA
A: RASIGUES: 9:244 < NRX-
A: RESIGUES: 9:244 < NRX-
A: CROSS-references: EMBL::651556; NID::947291; PIDN:CAN43754.1; PID::947292
A: CROSS-references: EMBL::651556; NID::947291; PIDN:CAN43754.1; PID::947292
A: RACCOSS: The nucleotide sequence was submitted to the EMBL Data Library, Septemb
A: Accession: S18785
A: Accession: S18785
A: Accession: S18785
A: CROSS-references: EMBL::65159; NID::947293; PIDN::CAN43757.1; PID::947294
A: CROSS-references: EMBL::65159; NID::947294; PIDN::CAN43757.1; PID::947294
A: CROSS-References: EMBL::947294; PIDN::PID::947294; PIDN::PID::947294; PIDN::PID::947294; PIDN::PID::947294; PIDN::PID::947294; PIDN::PID::947294; PIDN::PID::947294;
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A: Cross references: EMBL::A61555; NID:947309; PIDN:CAM43753.1; PID:947310

A: EXperimental source: Streptococcus pyogenes strain MGA827 isolate Arisona unassign A: Rote: the nuclectide sequence was submitted to the EMBL Data Library, September 199

A: Accession: SIB796

A: Strains: nuclection and sequence not shown; translation not shown

A: Strains: nuclection

A: Residues: 9-744 * MRD:

A: Residues: 9-744 * MRD:: X61557; NID:947319; PIDN:CAM43755.1; PID:947320

A: Cross-references: EMBL:: X61557; NID:947319; PIDN:CAM43755.1; PID:947320

A: Residues: 9-744 * MRD:: X61557; NID:947319; PIDN:CAM43755.1; PID:947320

A: Residues: NID:940 * MRD:: X61557; NID:947319; PIDN:CAM43755.1; PID:947320

A: Residues: NID:940 * MRD:: X61557; NID:947319; PIDN:CAM43755.1; PID:947320

A: Residues: NID:940 * MRD:: X61557; NID:947319; PIDN:CAM43755.1; PID:947320

A: Residues: NID:940 * MRD:: X61557; NID:947319; PIDN:CAM43755.1; PID:947320

A: Residues: NID:940 * MRD:: X61557; NID:947319; PIDN:CAM43755.1; PID:947320

A: Residues: NID:940 * MRD:: X61557; NID:947319; PIDN:CAM43755.1; PID:947320

A: Residues: NID:940 * MRD:: X61557; NID:947319; PIDN:CAM43755.1; PID:947320

A: Residues: NID:940 * MRD:: X61557; NID:947319; PIDN:CAM43755.1; PID:947320

A: Residues: NID:940 * MRD:: X61557; NID:947319; PIDN:CAM43755.1; PID:947320

A: Residues: NID:940 * MRD:: X61557; NID:947319; PIDN:CAM43755.1; PID:947320

A: Residues: NID:940 * MRD:: X61557; NID:947319; PIDN:CAM43755.1; PID:947320

A: Residues: NID:940 * MRD:: X61557; NID:947319; PIDN:CAM43755.1; PID:947320

A: Residues: NID:940 * MRD:: X61557; NID:947319; PIDN:CAM43755.1; PID:947320

A: Residues: NID:940 * MRD:: X61557; NID:947319; PIDN:CAM43755.1; PID:947320

A: Residues: NID:940 * MRD:: X61557; NID:947319; PIDN:CAM43755.1; PID:947320

A: Residues: NID:940 * MRD:: X61557; NID:947319; PIDN:CAM43755.1; PID:947320

A: Residues: NID:940 * MRD:: X61557; NID:947319; PIDN:CAM43755.1; PID:947320

A: Residues: NID:940 * MRD:: X61557; NID:947319; PIDN:CAM43755.1; PID:
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A; Molecule Type: DNA
A; Res fulues: 9-218 <MRS>
A; Res fulues: 9-218 <MRS>
A; Res fulues: 9-218 cmS>
A; Cross references: EMBL: X61554; NID: 947327; PIDN: CAAA3752.1; PID: 947328
A; Experimental source: Streptococcus pyogenes strain MGAS500 isolate New Zealand unas
A; Experimental source: Streptococcus pyogenes strain MGAS500 isolate New Zealand unas
A; Experimental source: Streptococcus pyogenes strain MGAS500 isolate New Zealand unas
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A.Cross-references: EMBL.X61559; NID:847293; PIDN:CAM43757,1.1 PID:947294
A.HOCE: the nucleocide sequence was submitted to the EMBL Data Library, September 199
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F;1-30/Domain: signal sequence #status
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SFWFDFFPEPEFTQSKYLMIYKDNETLDSNTSQIEVYLTTK
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Pred. No. 7.
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to the EMBL Data Library, September
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A: Molecule type: DNA
A: Residues; 1236 < NREY
A: Residues; 1236 < NREY
A: Cross references: EMBL: X61572; NID:947333; PIDN:CAA43770.1; PID:947334
A: Experimental source: Strain MGAS624 isolate Germany unassigned phage
A: Mote: the nucleotide sequence was submitted to the EMBL Data Library, Septi
A: Accession: S18798
A: Status: nucleic acid sequence not shown; translation not shown
A: Molecule type: DNA
A: Residues: 1-236 < KRED
A: Cross : references: EMBL: X61571; NID:947323; PIDN:CAA43769.1; PID:947324
A: Experimental source: strain MGAS495 isolate Germany unassigned phage
A: Note: the nucleotide sequence was submitted to the EMBL Data Library, Septi
C: Genetics:
A: Gene: spea3
C: Superfmaily: enterotoxin B
C: Keywords: exotoxin
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A:Folscibles: 1236 <REZ>
A:Cross-references: EMBL:X61570; NID:947315; PIDN:CAN43768.]; PID:947316
A:Experimental source: Extain MASS91 isolate United Kingdom unassigned;
A:More: the nucleotide sequence was submitted to the EMBL Data Library,
A:Note: the nucleotide sequence was submitted to the EMBL Data Library,
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A: Gross: references: EMBL: X61569; NID: 947313; PIDN: CAA43767.1; PID: 947314
A: Experimental source: strain MGAS485 isolate rugoslavia unassigned phag
A: More: the nucleotide sequence was submitted to the EMBL Data Library,
A: Accession: S18794
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J. Exp. Med. 174, 1271-1274, 1991
A:7itle: Characterization and clonal distribution of four alleles
A:Reference number: S18782; MUID:92044323; PMID:1940804
A:Accession: S18783
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A:Experimental source: Exraîn M632158 isolate Nebraska unassigned phoe
A:Note: the nucleotide sequence was submitted to the EMBL Data Library,
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A; Residues: 1-236 <NEL>
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                                                                                 181
                                                                                                                                                                                                                             121 VSIDGIQSLSFDIETNKKMYTAQELDYKVRKYLTDNKQLYTNGPSKYETGYIKFIPKNKE 180
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                                        SFWFDFFPEPEFTQSKYLMIYKDNETLDSNT
                                                                                                                                                       VSIDGIQSLSFDIETNKKMYTAQELDYKYRKYLTDNKQLYTNGPSKYETGYIKFIPKNKE
                                                                                                                                                                                                                                                                                                              ELKNQEMATLFKDKNIDIYGVEYYHLCYLCENAERSACIYGGVTNHEGNHLEIPKKIVVK 142
                                                                                                                                                                                                                                                                                                                                                       ELKNOEMATLFKDKNIDIYGVEYYHLCYLCENAERSACI-GGVTNREGNHLEIPKKIVVK 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QQDPDPSQLHRSSLVKNLQNIYFLYBGDPVTHENVKSVDQLRSHDLIVNVSGPNYDKLKT
SEWEDEFPEFTQSKYLMIYKDNETLDSNT
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Pred. No. 9.3e-65;
0; Mismatches 2; Indels 1;
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N;Alternate names: scarlet fever toxin
C;Species: Streptococcus pyogenes phage
A;Variety: strain MGAS250 isolate California; strain MGAS251 isolate California;
Isolate United Kingdom; strain MGAS466 isolate Germany
C;Date: 29-3na-1993 #sequence_revision 29-3na-1993 #text_Change 16-Jul-1999
C;Date: 29-3na-1993 #sequence_revision 29-3na-1993 #text_Change 16-Jul-1999
C;Accession: S18786; S18787; S18788; S18799; S18792; S18795; S18799

R; Nelson, Nelson, K.; Schlievert, P.M.; Selander, R.K.; Musser, Exp. Med. 174, 1271-1274, 1991

A.71tle: Characterization and clonal distribution of four alleles A,Reference number: S18782; MUID:92044723; PMID:1940804 A,Accession: 518786 ç the speA

gene

en

acid sequence not shown; translation not shown

A;Status: nucleic acid A;Molecule type: DNA A;Residues: 1-236 <NEL>

A:Cross-references: EMBL:K61561, NID:407297; FID:8:CAB43759 1; FID:947298
A:Experimental source: Strain M638250 isolate California unassigned phage
A:Experimental source: Strain M638250 isolate California unassigned phage
A:Note: the nucleocide sequence was submitted to the EMBL Data Library, September A; Accession: S18787

A; Molecule type: DNA A; Status: nucleic acid sequence not shown; translation not shown

A; Residues: 1-236 <NEA>

September

A;Cross:references: EMBL:X61562; NID:q47299; PIDN:CAA43760.1; PID:q47300
A;Experimental source: strain MGAS221 isolate California unassignd phage
A;Acceston: S18788
A;Acceston: S18788
A;Status: notelet acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-236 <AREA
A;Residues: 1-236 <AREA
A;Residues: 1-236 <AREA
A;Residues: 1-236 <AREA
A;Cross:references: EMBL:X61563; NID:q47301; PIDN:CAA43761.1; PID:q47302
A;Experimental source: strain MGAS236 isolate California unassigned phage
A;Mote: the nucleotide sequence was submitted to the EMBL Data Library. A phage

A; Molecule type: DNA A; Residues: 1-236 <NEY> A;Accession: S18790
A;Status: nucleic acid sequence not shown; translation not shown

A; Cross: references: EMBL:X61564, NID:407305, PIDM:CAA43762.1, PID:947306 A; Experimental source: Strain MGAS285 isolate Colorado unassigned phage A; Note: the nucleotide sequence was submitted to the EMBL Data Library,

A;Accession: S18792 A;Status: nucleic acid sequence September

199

not

shown; translation not shown

A:Molecule type: DNA
A:Residues: 1-226 <NBO
A:Residues: 1-226 <NBO
A:Cross-references: EMBL:K61565; NID:g47311; PIDN:CAA43763.1; PID:g47312
A:Experimental source: EMBL:K61565; NID:g47311; PIDN:CAA43763.1; PID:g47312
A:Experimental source: EMBL:M615480 isolate Yugoslavia unassigned phag
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, A; Status: nucleic acid sequence not A; Accession: S18795 shown; translation not shown phage ary, September 199

A; Note: the nucleotide sequence was submitted A:Molecule type: DNA A:Residues: 1-256 (AUE)> A:Cross-references: EMBL:X61566; NID:g47317; PIDN:CAA43764.1; PID:g47318 A:Experimental source: strain MGAS492 isolate United Kingdom unassigned United Kingdom unassigned to the EMBL Data Library, phage September 199

A; Molecule type: DNA A; Residues: 1-236 <NES> A; Status: nucleic acid sequence not A; Accession: S18799 shown; translation not

A;Cross-references: EMBL:X61567, NID:q47325, PIDN:QAM43765.]; PID:q47326 A;Experimental source: strain MGA5496 isolate Germany unassigned phage A;Note: the nucleotide sequence was submitted to the EMBL Data Library, C; Genetics: Germany unassigned phage to the EMBL Data Library EMBL Data Library,

September 199

C; Superfamily: A; Gene: speA2 enterotoxin

F;1-22/Domain: signal sequence (fragment) #status predicted <SIG>F;23-236/Product: exotoxin type A (fragment) #status predicted <M. C;Keywords: exotoxin F;1-22/Domain: signa **MAT**

Ş Query Match Best Local Matches Similarity 43.68; Score 1089.5; Pred. No. 2.7e Mismatches 2.7e-64; DB 2; Indels Length 236; ۲ Gaps

RESULT 5 S18786

exotoxin type

×

precursor

(allele

2)

Streptococcus pyogenes

phage

(strain

MGAS250

밁 23 2 QQDPDPSQLHRSSLVKNLQNIYFLYEGDPVTHENVKSVDQLRSHDLIYNVSGPNYDKLKT 61

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A: Molecule type: DNA
A: Residues: 1-236 <REL
A: Cross-references: EMBL:X61573; NID:947303; PIDN:CANA3771.1; PID:947304
A: Cross-references: EMBL:X61573; NID:947303; PIDN:CANA3771.1; PID:947304
A: Note: the nucleotide sequence was submitted to the EMBL Data Library, (
C: Genetics:
A: Gene: speA
C: Superfamily: enterotoxin B
C: Superfamily: enterotoxin B
C: Keywords: exotoxin
F:1-22/Domain: signal sequence (fragment) #status predicted <NAT>
---7-746/Dornduct: exotoxin A (fragment) #status predicted <NAT>
     streptococcal pyrogenic evotoxin type A precursor - Streptococcus sp. N.Alternate names: scanlet fever toxin; SPE type A (Streptococcus sp. Cipoccias: Streptococcus sp. Cipoccias: Scanley Streptococcus sp. Cipoccias: Scanley Streptococcus sp. Cipoccias: Scanley Streptococcus sprogenic sp. Scanley Streptococcus sprogenic sp. Cipoccias: Streptococcus sprogenic sp. Cipoccias: Addisor Addisors Addisors Addisors Addisors Addisors Addisors Addisors Streptococcus sp. Cipoccias: Addisors Addisors Addisors Addisors Streptococcus sp. Cipoccias: Addisors Addisors Addisors Addisors Addisors Addisors Streptococcus sp. Cipoccus Streptococcus sp. Cipoccias Streptococcus sp. C
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C:Species Streptococcus pyogenes
A:Varlety: strain MGAS262 isolate Callfornia
C:Date: 29-Jan-1993 *text_change
C:Date: 29-Jan-1993 *text_change
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J. Exp. Ned. 174, 1271-1274, 1991
A;Title: Characterization and clonal distribution of four alleles
A;Reference number: S18782; MUID:92044323; PMID:1940804
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exotoxin A precursor (allele 4) - Streptococcus pyogenes
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A; Status: nucleic acid sequence not shown;
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A. Residue: 28-55, NMD; 59-68 'NE',71, 'FDLIYL',78-117,119-127,'N',129,'D',131-
A. Residue: 28-55, NMD; 59-68 'NE', 51-68
R. Hunny, I.V.; Bergdoll, M.S., 1970
J. Biol. Chem. 245, 3511-3517, 1970
J. Biol. Chem. 245, 3511-3517, 1970
A. Reference number: A2906; MUD:71007901; PMID:5470820
A. Contents: annotation; chymotryptic peptides
A. Contents: annotation; chymotryptic peptides
R. Runny, I.V.; Bergdoll, M.S.
R. Hunny, I.V.; Bergdoll, M.S.
R. Reference number: A29063; MUD:71007900; PMID:5470819
A. Contents: annotation; tryptic peptides
R. Schantz, B.J.; Rossaler, M.G.; Ragman, J.; Sporo, L.; Dunnery, D.A.; Bergdoll M.S. Reference number: A90548; MUD:60035792; PMID:453912
A. Reference number: A90548; MUD:60035792; PMID:4593912
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A; Residues: 1-266 < JON>
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A; Residues: 1-250 <JOH>
C; Superfamily: enterotoxin
C; Keywords: exotoxin
                                                                                                                             124 DGIQSLSFDIETNKKMVTAQELDYKVRKYLTDNKQLYTNGPSKYETGYIKFIPKNKESFW 183
                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                    DGIQSLSFDIEQIKN-GNCSRISYTVRKYLTDNKQLYTNGPSKYETGYIKFIPKNKESFW 212
                                                                                                                                                                            NQEMATLFKDKNVDIYGVEYYHLCYLCENAERSACLYGGVTNHEGNHLEIPKKIVVKVSI 153
                                                                                                                                                                                                     NQEMATLFKDKNIDIYGVEYYHLCYLCENAERSACI-GGVTNREGNHLEIPKKIVVKVSI 123
                                                                                                                                                                                                                                                                                                            PDPSQLHRSSLVKNLQNIYFLYEGDPVTHENVKSVDQLRSHDLIYNVSGPNYDKLKTELK
                                                                                                                                                                                                                                                                   PKPSQLQRSNLVKTFKIYIFFMRVTLVTHENVKSVDQLLSHDLIYNVSGPNYDKLKTELK
FDFFPEPEFTQSKYLMIYKDNETLDSNTSQIEVYLTTK 250
                     FDFFPEPEFTQSKYLMIYKDNETLDSNT-QIEVYLTTK 220
                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                             37.5%;
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                                                                                                                                                                                                                                                                                                                                                        Score 938.5; DB 1;
Pred. No. 2.3e-54;
5; Mismatches 25;
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B precursor - Staphylococcus aureus

A;Title: Nucleotide sequence of the enterotoxin B gene from Staphylococcus aureus A;Reference number: \$27360; NUID:86168029; PMID:3957869 C:Species: Staphylococcus sureus
C:Date: 24-Apr.1994 #sequence_revision 15-Oct-1996 #text_change 18-Jun-1999
C:Accession: S27360; A92065; S27240; A01815
C:Jones, C.L.; Khang S.A.
J. Bacteriol. 166, 29-33; 1986

A; Experimental source: strain S6 A;Cross-references: EMBL:M11118; NID:g152999; PIDN:AAA88550.1; PID:g153000

R; Hunng, I.Y.; Bergdoll, M.S.
J. Blol. Chem. 245, 3518-3525, 1970
A; Title: The primary structure of staphylococcal enterotoxin A; Reference number: A92065; MUID:71007902; PMID:5470821
A; Accession: A92065 В. III. The cyanogen bro

,131-132,

Isolation,

compos

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Dunnery, D.A.; Bergdoll, Isolation, composi

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A:Tille: Identification of functionally active fragments A:Paference number: S27240; MUID:93049338; PMID:1425690 A; Reference number: \$27240; MUID: 93049338; A; Accession: \$27240 Maurer-Fogy, I.; Moskaleva, of. staphylococcal enterotoxi E.Y.; Sves

A; Molecule type: protein
A; Mesidues; 28-42; 128-138 - ALA>
C; superfamily: enterctoxin; extracellular protein; toxin
C; Koywords: enterotoxin; extracellular protein; toxin
F; 1-27/Domain: signal sequence istatus predicted <SIG>

Tue

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enterotoxin G-2 precursor - Staphylococcus aureus
N;Alternate names; enterotoxin G-2 precursor
C:Specias: Staphylococcus aureus
C:Dates: 10.Nov-1992 *sequence_revision 10.Nov-1992 *text_c
C:Dates: 10.Nov-1994 *sequence_revision 10.Nov-1992 *text_c
C:Accession: A60114; B6014; A33866
R:Bobach, G.; Schilerett, P.M.
A:Title: Conservation of the biologically active portions
A:Rithe: Conservation of the biologically active portions
A:Reference number: A6014; MUD:89277549; PMID:2243637
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C:species: Staphylococcus aureus
C:species: 19:Mar:1997 #sequence_revision 19:Mar:1997 #text_change 16:Jul-1999
C:Accession: 19:Mar:1997 #sequence_revision 19:Mar:1997 #text_change 16:Jul-1999
C:Accession: 19:Mar:1997 #sequence_revision 6:A.
R:iOvide: C.J.; Hankett, S.P.; Bohach, G.A.
R:iOvide: C.J.; Hankett, S.P.; Bohach, G.A.
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A;Title: Nucleotide sequence of the staphylococcal enterotoxin
A;Reference number: S11885; MUID:90220508; PMID:3325627
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A; Residues: 1-266 <HOV>
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F;120-140/Disulfide bonds: #status experimental
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                         111 LEIP--KKIVVKVSIDGIQSLSFDIETNKKMVTAQELDYKVRKYLTDNKQLYTNGPSKYE 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            108 GNHLEIPKKIVVKVSIDGIQSLSFDIETNKKMYTAQELDYKVRKYLTDNKQLYINGPSKY 167
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            90
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QPDPMPDDLHKSSEFTGTMGNMKYLYDDHYVSATKVKSVDKFLAHDLIYNISDKKLKNYD 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QQDPDPSQLHRSS-LYKNLQNIYFLYEGDPVTHENYKSVDQLRSHDLIYNYSG---PNYD 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ETGYIKFIPKNKESFWFDFFPEP -- EFTQSKYLMIYKDNETLDS-NTQIEVYLTTKQ 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GNQLDKYRSITVRVFEDGKNLLSFDVQTNKKKVTAQELDYLTRHYLVKNKKLYEFNNSPY 209
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QPDPKPDELHKSSKFTGLMENMKVLYDDNHVSAINVKSIDQFLYFDLIYSIKDTKLGNYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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Pred. No. 1.9e-26;
Pred. No. 1.9e-26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 541; DB 1;
Pred. No. 2.8e-28;
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                                                                                                                   10-Nov-1992 #text_change 16-Jul-1999
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                         of staphylococcal enterotoxins
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C;Superfamily: enterotoxin B F;1-27/Domain: signal sequence #status predicted F;1-27/Domain: signal sequence #status predict F;28-266/Product: enterotoxin C-2 #status predict
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A;Status: not compared with conceptual translation
A;Molecule type: DNA
A;Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Residues: 1-266 <COU>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Accession: A33866
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Title: Nucleotide sequence of the type C-3 staphylococcal enterotoxin gene suggests A;Reference number: A33866; MUID:89327174; PMID:2473979
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R; Couch, J.L.; Betley, M.J.
J. Bacteriol. 171, 4507-4510,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: protein A; Residues: 28-66 < BOH2>
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Best Local
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210
                                    169
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TGYIKFIENNGNTFWYDMMPAPGDKFDQSKYLMMYNDNKTVDSKSVKIEVHLTTK
                                                                            FDNGNLQNVL1RVYENKRNT1SFEVQTDKKSVTAQELD1KARNFL1NKKNLYEFNSSPYE
                                                                                                                                                                                                  KLKTELKNQEMATLFKDKNIDIYGVEYYHLCYLCE-----NAERSACIGGVTNREGNH 110
                                                                                                                                                                                                                                                                               QQDPDPSQLHRSS-LVKNLQNIYFLYEGDPVTHENVKSVDQLRSHDLIYNVSG----PNYD 57
                                 TGYIKFIPKNKESFWEDFFPEP--EFTQSKYLMIYKDNETLDS-NTQIEVYLTTK
                                                                                                                                                           KVKTELLNEDLAKKYKDEVVDVYGSNYYVNCYFSSKDNVGKVTGGKTCMYGGITKHEGNH
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                                                                                                                                                                                                                                                                                                                                                              Score 510;
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                                                                                                                                                                                                                                                                                                                                             Pred. No. 3e-26;
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                DB 2;
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264
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enterotoxin C-1 precursor - Staphylococcus aureus C;Species: Staphylococcus aureus

C; Accession: S06356; A01816 R; Bohach, G.A.; Schlievert, P.M. C;Date: 15-Nov-1984 #sequence_revision 05-Jan-1996 #text_change 18-Jun-1999

Mol. Gen. Genet. 209, 15-20, 1987
A.Fitle: Nucleotide sequence of the staphylococcal enterotoxin Cl
A.Feterence number: S06356; MUID:88038352; PMID:2823067
A.Fecession: S06356

gene

and

relatednes

A; Molecule type: DNA A; Residues: 1-266 <BOH>

R;Schmidt, J.J.; A;Cross-references: EMBL:X05815; NID:g46566; PIDN:CAA29260.1; PID:g46567 Spero,

enterotoxin

2

J. Biol. Chem. 258, 6300-6306, 1983 A; Title: The complete amino acid see A; Reference number: A01816; MUID:83 acid sequence of Staphylococcal MUID:83213327; PMID:6189824

A;Molecule type: protein A;Residues: 28-75,'IL',78-176,'N',178-266 <SCH> A; Accession: A01816

A;Gene: entC1 · C; Genetics:

C; Keywords: enterotoxin C; Superfamily: enterotoxin

F;1-27/Domain: signal sequence *status predicted F;28-266/Product: enterotoxin C-1 *status experimental F;120-137/Disulfide bonds: *status experimental #status experimental <SIG CMATS

Query Match

20.48;

Score

509;

В ::

Length 266;

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cysteine proteinase (EC 3.4.22.-) / hemagglutinin protein - Porphyromonas gingivalis C;Species: Porphyromonas gingivalis C;Species: Foul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999 C;Botte: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999 #sequence_revision 16-Jul-1999 #sequence_revision 16-Ect. Immunc. 63, 238-247, 1995 #sequence of the Porphyromonas gingivalis prtT cysteine protease/hcmm A;Refergace number: 217199; MUID:95105001; PMID:7806362
                                                                                                                                            RESULT 13
T10890
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C.: Shlba, T.: Hattori, M.; Ögasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 128-1240, 2001
A.Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus.
A:Reference number: A89758; MUID:21311952; PMID:11418146
A:Accession: 689968
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C;Superfamily: enterotoxin B
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A.Residues: 1-258 <KUR>
A.Gross-references: GB.BA000018; PID:g13701617; PIDN:BAB42910.1; GSPDB:GN00149
A.Gross-references: Strain N315
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Best Local :
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hes 105; Conser
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                                                                                                                                                                                                                                                                                                                                                                               58 KLKTELKNOEMATLFKDKNIDIYGVEYYHLCYLCE----NAERSAC--IGGVTNREGNH
                                                                                                                                                                                                                                                                                                                                                                                                                    26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      101;
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                                                                                                                                                                                                                                                                                                                                                                                                                                              2 QQDPDPSQLHRSSLVKN----LQNIYFLYEGDPVTHENVKSVDQLRSHDLIYNVSGPNYD
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                                                                                                                                                                                                                              YIKFIPKNKESFWFDFFPEPE---FTQSKYLMIYKDNETLDSNT-QIEVYLTT 219
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YIKFTEKNNTSFWFDLFPKKELVPFVPYKFLNIYGDNKVVDSKSIKMEVFLNT
                                                                                                                                                                                                                                                                                                                                              EVKTELENTELANNYKDKKVDIFGVPYFYTCIIPKSEPDINQNFGGCCMYGGLTFNSSEN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TGYIKFIPKNKESFWFDFFPEP--EFTQSKYLMIYKDNETLDS-NTQIEVYLTTK 220
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QQDPDPSQLHRSSLVKNL-QNIYFLYEGDPVTHENVKSVDQLRSHDLIYNVSG---PNYD
                                                                                                                                                                                                                                                                            -ERDKLITVQVTIDNRQSLGFTITTNKNMVTIQELDYKARHWLTKEKKLYEFDGSAFESG
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43.3%; Pred. No. 6.1e-22;
111ve 37; Mismatches 79
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4; Mismatches 70;
       onas gingivalis prtT cysteine protease/hemagg PMID:7806362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2; Length 258;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 79;
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enterotoxin YEN72 (imported] - Staphylococcus aureus (strain N315)
C:Spate: 10-May-2001 sequence_revision 10-May-2001 *text_change 22-Oct-2001
C:Accession: A89269
R:Kurodb, M.; Ohta, T.; Uchityama, I.; Babb, T.; Yuzawa, H.; Kobayashi, I.; Cui, I.;
ma, A.; Mituani-Ui, Y.; Kobayashi, N.; Savano, T.; Inoue, R.; Kalto, C.; Sekimizu,
Lancet 337, 1235-1240, 2001
A:Reference number: A89758; MOID:21311932; PMID:11418146
A:Reference number: A89758; MOID:21311932; PMID:11418146
                                                                                                                                                                                                                                                              A; Gene:
                                                                                                                                                                                                                                                                                A; Experimental source:
C; Genetics:
                                                                                                                                                                                                                                                                                                     A;Cross-references: GB:BA000018; PID:g13701619; PIDN:BAB42912.1; GSPDB:GN00149
A;Experimental source: strain N315
                                                                                                                                                                                                                                                                                                                                               A; Molecule type: DNA
A; Residues: 1-136 < KUR>
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C; Keywords:
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C;Genetics:
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A;Status: preliminary; translated
A;Molecule type: DNA
A;Residues: 1-886 <MAD>
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Best Local S
Matches 94
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            230 SKGIHYNQGNPYNLLTPVIEKVKPGEQSFVGQHAATGCVATATAQIMKYHNYPNKGLKDY
62
                                                                                                                                95
                                                                                2 KKTCMYGGVTEHDGNQIDKNNSTDNSHNILIKVYENERNSLSFDIPTNKKNITAQEIDYK 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cysteine proteinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         G
VRNYLLKHKNLYEFNSSPYETGYIKFIEGSGHSFWYDLMPESGKKFYPTKYLLIYNDNKT
                                                                                                        ERSACIGGVTNREGNHL-----EIPKKIVVKVSIDGIQSLSFDIETNKKMVTAQELDYK 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DYGPSSGSAGSSRVQRALKENFGYNQSVHQINRSDF-SQDWEAQIDKELSQNQPVYYQGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DGSMGHAFVCDGYEPDGTFHFNWGWGGMSNGNFYLNLLNPGSLGTGAGDGGYSTDQEVVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KVG-GHAFVIDGADGRNFYHVNWGWGGVSDGFFRLDALNPSALGTGGGAGGFNGYQSAVV 467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QFADFGSGTFSIFVERALRETFHYKKSLRYIHRSLLPGKEWKDMIRKELAENRPVYYAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DYYDDMTGTH-THYSGTFG----ETYNWSKMPGNISVGISPEEVKALSTFMRDVSFSVNM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYTLSSNNPYFNHPKNLFAAISTRQYNWNNILPTYSGRESNVQKMAISELMADVGISVDM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SDPILWDQGYPFNTLHPLLPS-----GQQAYTGCVATAMGQIMRHYKWPEKASGEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  468
                                                                                                                                                                    12.1%; Score 303.5; DB ; ilarity 47.4%; Pred. No. 3.9e-13; Conservative 23; Mismatches 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL: S75942; NID: g913136; PID: g913137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16.9%; Score 422; 39.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hemagglutinin; hydrolase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              le-19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BG
                                                                                                                                                                                                              DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2; Length 886;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         94;
                                                                                                                                                                    Indels
                                                                                                                                                                                                              Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         <u>16</u>;
                                                                                                                                                                    9;
                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         399
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122

VESKSINVEVHLTKK 136

207 LDSNT-QIEVYLTTK 220

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R:bayles. K.H.; Indolo, J.J.
J. Bacteriol. 171, 4799-4805, 1989
A:Title: Generic and molecular analyses of the gene encoding staphylococcal enterotoxin kneference number: A3953; NUID:89359112; PMID:2549000
A:Accession: A3953
A:Status: preliminary
A:Holecule type: DNA
A:Residues: 1-258 <BAY-
A:Cross-references: GB:R9521; NID:91492109; PIDN:AABB6195.1; PID:9758691
C:Superfamily: enterotoxin B
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enterotoxin D precursor - Staphylococcus aureus
C;Species: Staphylococcus aureus
C;Date: 09-Mar-1990 #sequence_revision 09-Mar-1990 #text_change 15-Oct-1999
                                                                                                                                                                                                                                                                                                                                               Ouery Match 11.8%; Score 295.5; DB 2; Length 258; Best Local Similarity 35.0%; Pred. No. 3.6-12; Matches 79; Conservative 44; Mismatches 68; Indels 17
213 SSDGSKVSYDLFDVKGDFPEKQLRIYSDNKTLSTEHLHIDIYLYEK 258
                                                                              176 PKNKESFWEDEFFDEPEFTQSKYLMIYKDNETLDS-NTQIEVYLTTK 220
                                                                                                                                                                   94 INFNSKEMAQHEKSKNYDYYPIRYSINCYGGE-IDRTACTYGGYTPHEGNKLKERKKIPI 152
                                                                                                                                                                                              36 ELHKKSELSSTALNNMKHSY--ADKNPIIGENKSTGDQFLENTLLYKKFFTDLINFEDLL 93
                                                                                                                                                                                                                                                                                   9 OLHR-----SSLVKNIQNIYFLYEGDPVTHENVKSVDQLRSHDLIYN---VSGPNYDKLK 60 :||: ||: ||: ||: ||: ||: ||
                                                                                                                                                                                                                                                                                                                                            17; Gaps
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Search completed: June 23, 2003, 16:15:55 Job time: 35.4979 secs

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